

## SEQUENCE LISTING

- <110> Genentech, Inc.  
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Wood, William, I.
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- <150> US 60/145,698  
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- <150> US 60/146,222  
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- <150> PCT/US99/20594  
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- <150> PCT/US99/20944  
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Arg Cys Arg Gly Leu Val Asp Lys Phe Asn Gln Gly Met Val Asp Thr
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Ala Lys Lys Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Lys Thr
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Leu Ser Lys Tyr Glu Ser Ser Glu Ile Arg Leu Leu Glu Ile Leu Glu
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Gly Leu Cys Glu Ser Ser Asp Phe Glu Cys Asn Gln Met Leu Glu Ala
      85              90              95

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Gln Glu Glu His Leu Glu Ala Trp Trp Leu Gln Leu Lys Ser Glu Tyr
      100             105             110

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Pro Asp Leu Phe Glu Trp Phe Cys Val Lys Thr Leu Lys Val Cys Cys
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Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu  
 35 40 45

Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala  
 50 55 60

Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile

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|   |  | 85  |  | 90  |  | 95  |
| Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly |  |     |  |     |  |     |
|   |  | 100 |  | 105 |  | 110 |
| Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro |  |     |  |     |  |     |
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| His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln |  |     |  |     |  |     |
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| Gly Asn Thr Ile Leu Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr |  |     |  |     |  |     |
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| Asn Glu Arg Arg Ile Cys Glu Cys Pro Asp Gly Phe His Gly Pro His |  |     |  |     |  |     |
|   |  | 195 |  | 200 |  | 205 |
| Cys Glu Lys Ala Leu Cys Thr Pro Arg Cys Met Asn Gly Gly Leu Cys |  |     |  |     |  |     |
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| Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn |  |     |  |     |  |     |
|   |  | 225 |  | 230 |  | 235 |
| Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys |  |     |  |     |  |     |
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| Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln |  |     |  |     |  |     |
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| Ile Gly Lys Ser Lys Cys Lys Cys Ser Lys Gly Tyr Gln Gly Asp Leu |  |     |  |     |  |     |
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| Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys |  |     |  |     |  |     |
|   |  | 305 |  | 310 |  | 315 |
| His Glu Pro Asn Lys Cys Gln Cys Gln Glu Gly Trp His Gly Arg His |  |     |  |     |  |     |
|   |  | 325 |  | 330 |  | 335 |
| Cys Asn Lys Arg Tyr Glu Ala Ser Leu Ile His Ala Leu Arg Pro Ala |  |     |  |     |  |     |
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<213> Artificial Sequence

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<212> DNA

<213> Artificial Sequence

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<211> 164

<212> PRT

<213> Homo sapiens

<400> 12

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Pro Gly Leu His Leu Arg Gly Ile Arg Asp Ala Gly Gly Arg Tyr Cys  
 35 40 45

Gln Glu Gln Asp Leu Cys Cys Arg Gly Arg Ala Asp Asp Cys Ala Leu  
 50 55 60

Pro Tyr Leu Gly Ala Ile Cys Tyr Cys Asp Leu Phe Cys Asn Arg Thr  
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Val Ser Asp Cys Cys Pro Asp Phe Trp Asp Phe Cys Leu Gly Val Pro  
 85 90 95

Pro Pro Phe Pro Pro Ile Gln Gly Cys Met His Gly Gly Arg Ile Tyr  
 100 105 110

Pro Val Leu Gly Thr Tyr Trp Asp Asn Cys Asn Arg Cys Thr Cys Gln  
 115 120 125

Glu Asn Arg Gln Trp His Gly Gly Ser Arg His Asp Gln Ser His Gln  
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Pro Gly Gln Leu Trp Leu Ala Gly Trp Glu Pro Gln Arg Leu Leu Gly  
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His Asp Pro Gly

090505-071204

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<210> 15

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic  
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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic  
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<211> 960

<212> DNA

<213> Homo sapiens

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<211> 189

<212> PRT

<213> Homo sapiens

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Pro Pro Ser Leu Arg Cys Ser Leu His Ser Ala Cys Cys Ser Gly Asp
          35           40           45

Pro Ala Ser Tyr Arg Leu Trp Gly Ala Pro Leu Gln Pro Thr Leu Gly
 50           55           60

Val Val Pro Gln Ala Ser Val Pro Leu Leu Thr Asp Leu Ala Gln Trp
 65           70           75           80

Glu Pro Val Leu Val Pro Glu Ala His Pro Asn Ala Ser Leu Thr Met
          85           90           95

Tyr Val Cys Thr Pro Val Pro His Pro Asp Pro Pro Met Ala Leu Ser
          100          105          110

Arg Thr Pro Thr Arg Gln Ile Ser Ser Ser Asp Thr Asp Pro Pro Ala
          115          120          125

Asp Gly Pro Ser Asn Pro Leu Cys Cys Cys Phe His Gly Pro Ala Phe
          130          135          140

Ser Thr Leu Asn Pro Val Leu Arg His Leu Phe Pro Gln Glu Ala Phe
          145          150          155          160

Pro Ala His Pro Ile Tyr Asp Leu Ser Gln Val Trp Ser Val Val Ser
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Pro Ala Pro Ser Arg Gly Gln Ala Leu Arg Arg Ala Gln
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&lt;210&gt; 19

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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24

&lt;210&gt; 20

&lt;211&gt; 24

&lt;212&gt; DNA



<213> Homo sapiens

&lt;400&gt; 23

Met Gly Ala Ala Arg Leu Leu Pro Asn Leu Thr Leu Cys Leu Gln Leu  
 1 5 10 15

Leu Ile Leu Cys Cys Gln Thr Gln Tyr Val Arg Asp Gln Gly Ala Met  
 20 25 30

Thr Asp Gln Leu Ser Arg Arg Gln Ile Arg Glu Tyr Gln Leu Tyr Ser  
 35 40 45

Arg Thr Ser Gly Lys His Val Gln Val Thr Gly Arg Arg Ile Ser Ala  
 50 55 60

Thr Ala Glu Asp Gly Asn Lys Phe Ala Lys Leu Ile Val Glu Thr Asp  
 65 70 75 80

Thr Phe Gly Ser Arg Val Arg Ile Lys Gly Ala Glu Ser Glu Lys Tyr  
 85 90 95

Ile Cys Met Asn Lys Arg Gly Lys Leu Ile Gly Lys Pro Ser Gly Lys  
 100 105 110

Ser Lys Asp Cys Val Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr  
 115 120 125

Ala Phe Gln Asn Ala Arg His Glu Gly Trp Phe Met Ala Phe Thr Arg  
 130 135 140

Gln Gly Arg Pro Arg Gln Ala Ser Arg Ser Arg Gln Asn Gln Arg Glu  
 145 150 155 160

Ala His Phe Ile Lys Arg Leu Tyr Gln Gly Gln Leu Pro Phe Pro Asn  
 165 170 175

His Ala Glu Lys Gln Lys Gln Phe Glu Phe Val Gly Ser Ala Pro Thr  
 180 185 190

Arg Arg Thr Lys Arg Thr Arg Arg Pro Gln Pro Leu Thr  
 195 200 205

&lt;210&gt; 24

&lt;211&gt; 28

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 24

cagtacgtga gggaccaggg cgccatga

28

&lt;210&gt; 25

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| <400> 27    |            |            |            |            |            |      |
| acttgccatc  | acctgttgcc | agtgtggaaa | aattctccct | gttgaatttt | ttgcacatgg | 60   |
| aggacagcag  | caaagagggc | aacacaggct | gataagacca | gagacagcag | ggagattatt | 120  |
| ttaccatacg  | ccctcaggac | gttccctcta | gctggagttc | tggacttcaa | cagaacccca | 180  |
| tccagtcatt  | ttgattttgc | tgtttatttt | ttttttcttt | ttctttttcc | caccacattg | 240  |
| tatttttatt  | ccgtacttca | gaaatggggc | tacagaccac | aaagtggccc | agccatgggg | 300  |
| cttttttctc  | gaagtcttgg | cttatcattt | ccctgggggt | ctactcacag | gtgtccaaac | 360  |
| tccctggcctg | ccctagtgtg | tgcgctgcgc | acaggaacct | tgtctactgt | aatgagcgaa | 420  |
| gcttgacctc  | agtgctctct | gggatacccg | agggcgtaac | cgtactctac | ctccacaaca | 480  |
| accaaattaa  | taatgctgga | tttctgcgag | aactgcacaa | tgtacagtcg | gtgcacacgg | 540  |
| tctacctgta  | tggcaaccaa | ctggacgaat | tcccatgaa  | ccttcccaag | aatgtcagag | 600  |
| ttctccattt  | gcaggaaaac | aatattcaga | ccatttccag | ggctgctctt | gccagctct  | 660  |
| tgaagcttga  | agagctgcac | ctggatgaca | actccatact | cacagtgggg | gtggaagacg | 720  |
| gggccttccg  | ggaggctatt | agcctcaaat | tgttggtttt | gtctaagaat | cacctgagca | 780  |
| gtgtgectgt  | tgggcttcct | gtggacttgc | aagagctgag | agtggatgaa | aatcgaattg | 840  |
| ctgtcatatc  | cgacatggcc | ttccagaatc | tcacgagctt | ggagcgtctt | attgtggacg | 900  |
| ggaacctctc  | gaccaacaag | ggatcgcgc  | agggcacctc | cagccatctc | accaagctca | 960  |
| aggaattttc  | aattgtactg | aattcgtctg | cccaccctcc | tcccgatctc | ccaggtacgc | 1020 |
| atctgatcag  | gctctatttg | caggacaacc | agataaacca | cattcctttg | acagccttct | 1080 |
| caaattctgcg | taagctqgaa | cggctqgata | tatccaacaa | ccaactgcgg | atgctgactc | 1140 |

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<210> 28
<211> 660
<212> PRT
<213> Homo sapiens
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<400> 28
Met Gly Leu Gln Thr Thr Lys Trp Pro Ser His Gly Ala Phe Phe Leu
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Lys Ser Trp Leu Ile Ile Ser Leu Gly Leu Tyr Ser Gln Val Ser Lys
                20                      25                      30

Leu Leu Ala Cys Pro Ser Val Cys Arg Cys Asp Arg Asn Phe Val Tyr
          35                      40                      45

Cys Asn Glu Arg Ser Leu Thr Ser Val Pro Leu Gly Ile Pro Glu Gly
      50                      55                      60

Val Thr Val Leu Tyr Leu His Asn Asn Gln Ile Asn Asn Ala Gly Phe
  65                      70                      75                      80

Pro Ala Glu Leu His Asn Val Gln Ser Val His Thr Val Tyr Leu Tyr
                85                      90                      95

Gly Asn Gln Leu Asp Glu Phe Pro Met Asn Leu Pro Lys Asn Val Arg
          100                      105                      110

Val Leu His Leu Gln Glu Asn Asn Ile Gln Thr Ile Ser Arg Ala Ala
      115                      120                      125

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|            |     |     |     |     |     |     |     |     |     |     |     |     |     |     |            |
|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------------|
| Leu<br>130 | Ala | Gln | Leu | Leu | Lys | Leu | Glu | Glu | Leu | His | Leu | Asp | Asp | Asn | Ser        |
| Ile<br>145 | Ser | Thr | Val | Gly | Val | Glu | Asp | Gly | Ala | Phe | Arg | Glu | Ala | Ile | Ser<br>160 |
| Leu        | Lys | Leu | Leu | Phe | Leu | Ser | Lys | Asn | His | Leu | Ser | Ser | Val | Pro | Val<br>175 |
| Gly        | Leu | Pro | Val | Asp | Leu | Gln | Glu | Leu | Arg | Val | Asp | Glu | Asn | Arg | Ile<br>190 |
| Ala        | Val | Ile | Ser | Asp | Met | Ala | Phe | Gln | Asn | Leu | Thr | Ser | Leu | Glu | Arg        |
| Leu        | Ile | Val | Asp | Gly | Asn | Leu | Leu | Thr | Asn | Lys | Gly | Ile | Ala | Glu | Gly<br>220 |
| Thr<br>225 | Phe | Ser | His | Leu | Thr | Lys | Leu | Lys | Glu | Phe | Ser | Ile | Val | Arg | Asn<br>240 |
| Ser        | Leu | Ser | His | Pro | Pro | Pro | Asp | Leu | Pro | Gly | Thr | His | Leu | Ile | Arg<br>255 |
| Leu        | Tyr | Leu | Gln | Asp | Asn | Gln | Ile | Asn | His | Ile | Pro | Leu | Thr | Ala | Phe<br>270 |
| Ser        | Asn | Leu | Arg | Lys | Leu | Glu | Arg | Leu | Asp | Ile | Ser | Asn | Asn | Gln | Leu<br>285 |
| Arg<br>290 | Met | Leu | Thr | Gln | Gly | Val | Phe | Asp | Asn | Leu | Ser | Asn | Leu | Lys | Gln<br>300 |
| Leu<br>305 | Thr | Ala | Arg | Asn | Asn | Pro | Trp | Phe | Cys | Asp | Cys | Ser | Ile | Lys | Trp<br>320 |
| Val        | Thr | Glu | Trp | Leu | Lys | Tyr | Ile | Pro | Ser | Ser | Leu | Asn | Val | Arg | Gly<br>335 |
| Phe        | Met | Cys | Gln | Gly | Pro | Glu | Gln | Val | Arg | Gly | Met | Ala | Val | Arg | Glu<br>350 |
| Leu        | Asn | Met | Asn | Leu | Leu | Ser | Cys | Pro | Thr | Thr | Thr | Pro | Gly | Leu | Pro<br>365 |
| Leu<br>370 | Phe | Thr | Pro | Ala | Pro | Ser | Thr | Ala | Ser | Pro | Thr | Thr | Gln | Pro | Pro<br>380 |
| Thr<br>385 | Leu | Ser | Ile | Pro | Asn | Pro | Ser | Arg | Ser | Tyr | Thr | Pro | Pro | Thr | Pro<br>400 |
| Thr        | Thr | Ser | Lys | Leu | Pro | Thr | Ile | Pro | Asp | Trp | Asp | Gly | Arg | Glu | Arg        |

|       |     |
|-------|-----|
| <210> | 29  |
| <211> | 21  |
| <212> | DNA |

acttgagca agcggcgcg gcggagacag aggcagaggc agaagctggg gctccgtcct 60  
cgctcccac gacgatccc cgaggagagc cgcggccttc ggcgaggcga agagggcgac 120

|             |             |             |             |            |             |      |
|-------------|-------------|-------------|-------------|------------|-------------|------|
| gaggaagacc  | cgggtggctg  | cgccccctgcc | tcgcttccca  | ggcgccggcg | gctgcagcct  | 180  |
| tgccccctctt | gctcgcttg   | aaaatggaaa  | agatgctcgc  | aggctgcttt | ctgctgatcc  | 240  |
| tcggacagat  | cgtcctcctc  | cctgccgagg  | ccagggagcg  | gtcacgtggg | aggtccatct  | 300  |
| ctaggggag   | acacgctcgg  | accacccgc   | agacggccct  | tctggagagt | tcctgtgaga  | 360  |
| acaagcgggc  | agacctggtt  | ttcatcattg  | acagctctcg  | cagtgtcaac | acccatgact  | 420  |
| atgcaaaggt  | caaggagttc  | atcgtggaca  | tcttgcaatt  | cttggacatt | ggctctgatg  | 480  |
| tcacccgagt  | gggctgctc   | caatatggca  | gcactgtcaa  | gaatgagttc | tcctcaaga   | 540  |
| ccttcaagag  | gaagtccgag  | gtggagcgtg  | ctgtcaagag  | gatgcggcat | ctgtccacgg  | 600  |
| gcaccatgac  | tgggctggcc  | atccagtatg  | ccctgaacat  | cgcattctca | gaagcagagg  | 660  |
| gggcccggcc  | cctgagggag  | aatgtgccac  | gggtcataat  | gacgtgaca  | gatgggagac  | 720  |
| ctcaggactc  | cgtggccgag  | gtggctgcta  | aggcacggga  | cacgggcatc | ctaactcttg  | 780  |
| ccattggtgt  | gggccaggta  | gacttcaaca  | ccttgaagtc  | cattgggagt | gagccccatg  | 840  |
| aggaccatgt  | cttccttggtg | gccaatttca  | gccagattga  | gacgtgacc  | tcctgttcc   | 900  |
| agaagaagtt  | gtgcacggcc  | cacatgtgca  | gcacctgga   | gcataactgt | gccacttct   | 960  |
| gcacaaacat  | ccttggtca   | tacgtctgca  | ggtgcaaaaca | aggctacatt | ctcaactcgg  | 1020 |
| atcagacgac  | ttgcagaatc  | caggatctgt  | gtgccatgga  | ggaccacaac | tgtgagcagc  | 1080 |
| tctgtgtgaa  | tgtgccgggc  | tccttcgtct  | gccagtgtca  | cagtggctac | gccctggctg  | 1140 |
| aggatgggaa  | gaagtgtgtg  | gctgtggact  | actgtgcctc  | agaaaaccac | ggatgtgaac  | 1200 |
| atgagtgtgt  | aaatgctgat  | ggctcctacc  | tttgccagtg  | ccatgaagga | tttgctctta  | 1260 |
| accagatga   | aaaaacgtgc  | acaaggatca  | actactgtgc  | actgaacaaa | ccgggctgtg  | 1320 |
| agcatgagtg  | cgtcaacatg  | gaggagagct  | actactgccg  | ctgccaccgt | ggctacactc  | 1380 |
| tggaccccaa  | tggcaaaacc  | tgcagccgag  | tggaccactg  | tgcacagcag | gaccatggct  | 1440 |
| gtgagcagct  | gtgtctgaac  | acggaggatt  | ccttcgtctg  | ccagtgtca  | gaaggcttcc  | 1500 |
| tcacaaacga  | ggacctcaag  | acctgctccc  | gggtggatta  | ctgcctgctg | agtgaccatg  | 1560 |
| gttgtgaata  | ctcctgtgtc  | aacatggaca  | gatcctttgc  | ctgtcagtgt | cctgagggac  | 1620 |
| acgtgctccg  | cagcgatggg  | aagacgtgtg  | caaaattgga  | ctcttgtgct | ctgggggacc  | 1680 |
| acggtttgtga | acattcgtgt  | gtaagcagtg  | aagattcgtt  | tgtgtgccag | tgctttgaag  | 1740 |
| gttatatact  | cgtgaagat   | ggaaaaacct  | gcagaaggaa  | agatgtctgc | caagctatag  | 1800 |
| accatggctg  | tgaacacatt  | tgtgtgaaca  | gtgacgactc  | atacacgtgc | gagtgtctgg  | 1860 |
| agggattccg  | gctcgtgag   | gatgggaaac  | gctgccgaag  | gaaggatgtc | tgcaaatcaa  | 1920 |
| cccaccatgg  | ctgcgaacac  | atltgtgtta  | ataatgggaa  | ttcctacatc | tgcaaatgct  | 1980 |
| cagagggatt  | tgttctagct  | gaggacggaa  | gacggtgcaa  | gaaatgcact | gaaggcccaa  | 2040 |
| ttgacctggt  | ctttgtgatc  | gatggatcca  | agagtcttgg  | agaagagaat | tttgaggtcg  | 2100 |
| tgaagcagtt  | tgtcactgga  | attatagatt  | ccttgacaat  | ttccccaaa  | gccgctcgag  | 2160 |
| tggggctgct  | ccagtattcc  | acacaggtcc  | acacagagtt  | cactctgaga | aacttcaact  | 2220 |
| cagccaaaga  | catgaaaaaa  | gccgtggccc  | acatgaaata  | catgggaaag | ggctctatga  | 2280 |
| ctgggctggc  | cctgaaacac  | atgttttgaga | gaagttttac  | ccaaggagaa | ggggccaggc  | 2340 |
| ccctttccac  | aagggtgccc  | agagcagcca  | ttgtgttcac  | cgaaggacgg | gctcaggatg  | 2400 |
| acgtctccga  | gtgggccagt  | aaagccaagg  | ccaatgggat  | cactatgtat | gctgttgggg  | 2460 |
| taggaaaagc  | cattgaggag  | gaactacaag  | agattgcctc  | tgagcccaca | aacaagcatc  | 2520 |
| tcttctatgc  | cgaagacttc  | agcacaatgg  | atgagataag  | tgaaaaactc | aagaaaaggca | 2580 |
| tctgtgaagc  | tctagaagac  | tccgatggaa  | gacaggactc  | tccagcaggg | gaactgccaa  | 2640 |
| aaacgggtcca | acagccaaca  | gaatctgagc  | cagtaccat   | aaatatccaa | gacctacttt  | 2700 |
| cctgttctaa  | ttttgcagtg  | caacacagat  | atctgtttga  | agaagacaat | cttttacggg  | 2760 |
| ctacacaaaa  | gctttcccat  | tcaacaaaac  | cttcagggaag | cccttttgaa | gaaaaacacg  | 2820 |
| atcaatgcaa  | atgtgaaaac  | cttataatgt  | tccagaacct  | tgcaaacgaa | gaagtaagaa  | 2880 |
| aattaacaca  | gcgcttagaa  | gaaatgacac  | agagaatgga  | agccctggaa | aatcgcttga  | 2940 |
| gatacagatg  | aagattagaa  | atcgcgacac  | atltgtagtc  | attgtatcac | ggattacaat  | 3000 |
| gaacgcagtg  | cagagcccca  | aagctcaggc  | tattgttaaa  | tcaataatgt | tgtgaagtaa  | 3060 |
| aacaatcagt  | actgagaaac  | ctggtttgcc  | acagaacaaa  | gacaagaagt | atacactaac  | 3120 |
| ttgtataaat  | ttatctagga  | aaaaaatcct  | tcagaattct  | aagatgaatt | taccaggtga  | 3180 |
| gaatgaataa  | gctatgcaag  | gtatlttgta  | ataactgtg   | gacacaactt | gcttctgcct  | 3240 |
| catcctgcct  | tagtgtgcaa  | tctcatttga  | ctatacgata  | aagtttgcac | agtcttactt  | 3300 |



ctgtagaaca ctggccatag gaaatgctgt ttttttgtac tggactttac cttgatatat 3360  
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<211> 915

<212> PRT

<213> Homo sapiens

<400> 34

Met Glu Lys Met Leu Ala Gly Cys Phe Leu Leu Ile Leu Gly Gln Ile  
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Val Leu Leu Pro Ala Glu Ala Arg Glu Arg Ser Arg Gly Arg Ser Ile  
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Ser Arg Gly Arg His Ala Arg Thr His Pro Gln Thr Ala Leu Leu Glu  
 35 40 45

Ser Ser Cys Glu Asn Lys Arg Ala Asp Leu Val Phe Ile Ile Asp Ser  
 50 55 60

Ser Arg Ser Val Asn Thr His Asp Tyr Ala Lys Val Lys Glu Phe Ile  
 65 70 75 80

Val Asp Ile Leu Gln Phe Leu Asp Ile Gly Pro Asp Val Thr Arg Val  
 85 90 95

Gly Leu Leu Gln Tyr Gly Ser Thr Val Lys Asn Glu Phe Ser Leu Lys  
 100 105 110

Thr Phe Lys Arg Lys Ser Glu Val Glu Arg Ala Val Lys Arg Met Arg  
 115 120 125

His Leu Ser Thr Gly Thr Met Thr Gly Leu Ala Ile Gln Tyr Ala Leu  
 130 135 140

Asn Ile Ala Phe Ser Glu Ala Glu Gly Ala Arg Pro Leu Arg Glu Asn  
 145 150 155 160

Val Pro Arg Val Ile Met Ile Val Thr Asp Gly Arg Pro Gln Asp Ser  
 165 170 175

Val Ala Glu Val Ala Ala Lys Ala Arg Asp Thr Gly Ile Leu Ile Phe  
 180 185 190

Ala Ile Gly Val Gly Gln Val Asp Phe Asn Thr Leu Lys Ser Ile Gly  
 195 200 205

Ser Glu Pro His Glu Asp His Val Phe Leu Val Ala Asn Phe Ser Gln  
 210 215 220

Ile Glu Thr Leu Thr Ser Val Phe Gln Lys Lys Leu Cys Thr Ala His

0505056-071301

|                 |   |     |     |     |     |     |
|-----------------|---|-----|-----|-----|-----|-----|
| 225             |   | 230 |     | 235 |     | 240 |
| Met Cys Ser Thr | Leu Glu His Asn Cys Ala His Phe Cys Ile Asn Ile |     |     |     |     |     |
|                 | 245   |     | 250 |     |     | 255 |
| Pro Gly Ser Tyr | Val Cys Arg Cys Lys Gln Gly Tyr Ile Leu Asn Ser |     |     |     |     |     |
|                 | 260   |     | 265 |     |     | 270 |
| Asp Gln Thr Thr | Cys Arg Ile Gln Asp Leu Cys Ala Met Glu Asp His |     |     |     |     |     |
|                 | 275   |     | 280 |     |     | 285 |
| Asn Cys Glu Gln | Leu Cys Val Asn Val Pro Gly Ser Phe Val Cys Gln |     |     |     |     |     |
|                 | 290   |     | 295 |     |     | 300 |
| Cys Tyr Ser Gly | Tyr Ala Leu Ala Glu Asp Gly Lys Arg Cys Val Ala |     |     |     |     |     |
|                 | 305   |     | 310 |     | 315 | 320 |
| Val Asp Tyr Cys | Ala Ser Glu Asn His Gly Cys Glu His Glu Cys Val |     |     |     |     |     |
|                 | 325   |     | 330 |     |     | 335 |
| Asn Ala Asp Gly | Ser Tyr Leu Cys Gln Cys His Glu Gly Phe Ala Leu |     |     |     |     |     |
|                 | 340   |     | 345 |     |     | 350 |
| Asn Pro Asp Glu | Lys Thr Cys Thr Arg Ile Asn Tyr Cys Ala Leu Asn |     |     |     |     |     |
|                 | 355   |     | 360 |     |     | 365 |
| Lys Pro Gly Cys | Glu His Glu Cys Val Asn Met Glu Glu Ser Tyr Tyr |     |     |     |     |     |
|                 | 370   |     | 375 |     |     | 380 |
| Cys Arg Cys His | Arg Gly Tyr Thr Leu Asp Pro Asn Gly Lys Thr Cys |     |     |     |     |     |
|                 | 385   |     | 390 |     | 395 | 400 |
| Ser Arg Val Asp | His Cys Ala Gln Gln Asp His Gly Cys Glu Gln Leu |     |     |     |     |     |
|                 | 405   |     | 410 |     |     | 415 |
| Cys Leu Asn Thr | Glu Asp Ser Phe Val Cys Gln Cys Ser Glu Gly Phe |     |     |     |     |     |
|                 | 420   |     | 425 |     |     | 430 |
| Leu Ile Asn Glu | Asp Leu Lys Thr Cys Ser Arg Val Asp Tyr Cys Leu |     |     |     |     |     |
|                 | 435   |     | 440 |     |     | 445 |
| Leu Ser Asp His | Gly Cys Glu Tyr Ser Cys Val Asn Met Asp Arg Ser |     |     |     |     |     |
|                 | 450   |     | 455 |     |     | 460 |
| Phe Ala Cys Gln | Cys Pro Glu Gly His Val Leu Arg Ser Asp Gly Lys |     |     |     |     |     |
|                 | 465   |     | 470 |     | 475 | 480 |
| Thr Cys Ala Lys | Leu Asp Ser Cys Ala Leu Gly Asp His Gly Cys Glu |     |     |     |     |     |
|                 | 485   |     | 490 |     |     | 495 |
| His Ser Cys Val | Ser Ser Glu Asp Ser Phe Val Cys Gln Cys Phe Glu |     |     |     |     |     |
|                 | 500   |     | 505 |     |     | 510 |

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Tyr | Ile | Leu | Arg | Glu | Asp | Gly | Lys | Thr | Cys | Arg | Arg | Lys | Asp | Val |
|     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |
| Cys | Gln | Ala | Ile | Asp | His | Gly | Cys | Glu | His | Ile | Cys | Val | Asn | Ser | Asp |
|     |     | 530 |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |
| Asp | Ser | Tyr | Thr | Cys | Glu | Cys | Leu | Glu | Gly | Phe | Arg | Leu | Ala | Glu | Asp |
| 545 |     |     |     | 550 |     |     |     |     |     | 555 |     |     |     |     | 560 |
| Gly | Lys | Arg | Cys | Arg | Arg | Lys | Asp | Val | Cys | Lys | Ser | Thr | His | His | Gly |
|     |     |     |     | 565 |     |     |     |     | 570 |     |     |     |     | 575 |     |
| Cys | Glu | His | Ile | Cys | Val | Asn | Asn | Gly | Asn | Ser | Tyr | Ile | Cys | Lys | Cys |
|     |     |     | 580 |     |     |     |     | 585 |     |     |     |     | 590 |     |     |
| Ser | Glu | Gly | Phe | Val | Leu | Ala | Glu | Asp | Gly | Arg | Arg | Cys | Lys | Lys | Cys |
|     |     |     | 595 |     |     |     | 600 |     |     |     |     | 605 |     |     |     |
| Thr | Glu | Gly | Pro | Ile | Asp | Leu | Val | Phe | Val | Ile | Asp | Gly | Ser | Lys | Ser |
|     |     |     |     |     |     | 615 |     |     |     |     | 620 |     |     |     |     |
| Leu | Gly | Glu | Glu | Asn | Phe | Glu | Val | Val | Lys | Gln | Phe | Val | Thr | Gly | Ile |
| 625 |     |     |     |     | 630 |     |     |     |     | 635 |     |     |     |     | 640 |
| Ile | Asp | Ser | Leu | Thr | Ile | Ser | Pro | Lys | Ala | Ala | Arg | Val | Gly | Leu | Leu |
|     |     |     |     | 645 |     |     |     |     | 650 |     |     |     |     | 655 |     |
| Gln | Tyr | Ser | Thr | Gln | Val | His | Thr | Glu | Phe | Thr | Leu | Arg | Asn | Phe | Asn |
|     |     |     | 660 |     |     |     |     | 665 |     |     |     |     | 670 |     |     |
| Ser | Ala | Lys | Asp | Met | Lys | Lys | Ala | Val | Ala | His | Met | Lys | Tyr | Met | Gly |
|     |     | 675 |     |     |     |     | 680 |     |     |     |     | 685 |     |     |     |
| Lys | Gly | Ser | Met | Thr | Gly | Leu | Ala | Leu | Lys | His | Met | Phe | Glu | Arg | Ser |
|     |     |     |     |     |     | 695 |     |     |     |     | 700 |     |     |     |     |
| Phe | Thr | Gln | Gly | Glu | Gly | Ala | Arg | Pro | Leu | Ser | Thr | Arg | Val | Pro | Arg |
| 705 |     |     |     |     | 710 |     |     |     |     | 715 |     |     |     |     | 720 |
| Ala | Ala | Ile | Val | Phe | Thr | Asp | Gly | Arg | Ala | Gln | Asp | Asp | Val | Ser | Glu |
|     |     |     |     | 725 |     |     |     |     | 730 |     |     |     |     | 735 |     |
| Trp | Ala | Ser | Lys | Ala | Lys | Ala | Asn | Gly | Ile | Thr | Met | Tyr | Ala | Val | Gly |
|     |     |     | 740 |     |     |     |     | 745 |     |     |     |     | 750 |     |     |
| Val | Gly | Lys | Ala | Ile | Glu | Glu | Glu | Leu | Gln | Glu | Ile | Ala | Ser | Glu | Pro |
|     |     |     | 755 |     |     |     | 760 |     |     |     |     | 765 |     |     |     |
| Thr | Asn | Lys | His | Leu | Phe | Tyr | Ala | Glu | Asp | Phe | Ser | Thr | Met | Asp | Glu |
|     |     |     |     |     |     | 775 |     |     |     |     | 780 |     |     |     |     |
| Ile | Ser | Glu | Lys | Leu | Lys | Lys | Gly | Ile | Cys | Glu | Ala | Leu | Glu | Asp | Ser |
| 785 |     |     |     |     | 790 |     |     |     |     | 795 |     |     |     |     | 800 |

Asp Gly Arg Gln Asp Ser Pro Ala Gly Glu Leu Pro Lys Thr Val Gln  
805 810 815

Gln Pro Thr Glu Ser Glu Pro Val Thr Ile Asn Ile Gln Asp Leu Leu  
820 825 830

Ser Cys Ser Asn Phe Ala Val Gln His Arg Tyr Leu Phe Glu Glu Asp  
835 840 845

Asn Leu Leu Arg Ser Thr Gln Lys Leu Ser His Ser Thr Lys Pro Ser  
850 855 860

Gly Ser Pro Leu Glu Glu Lys His Asp Gln Cys Lys Cys Glu Asn Leu  
865 870 875 880

Ile Met Phe Gln Asn Leu Ala Asn Glu Glu Val Arg Lys Leu Thr Gln  
885 890 895

Arg Leu Glu Glu Met Thr Gln Arg Met Glu Ala Leu Glu Asn Arg Leu  
900 905 910

Arg Tyr Arg  
915

<210> 35

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 35

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23

<210> 36

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 36

acagccatgg tctatagctt gg

22

<210> 37

<211> 45

<212> DNA

<213> Artificial Sequence

0505056 074004

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

gcctgtcagt gtcttgaagg acacgtgctc cgcagcgatg ggaag

45

<211> 1813

<213> Home

<213> Homo sapiens

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| cggcacctgc  | aggtccgtgc | gtccccgggc | tggcgccct   | gactccgtcc | cggccaggga  | 120  |
| gggccaatgat | ttccctcccg | gggcccctgg | tgaccaactt  | gctgcggttt | ttgttctctgg | 180  |
| ggctgagtgc  | cctcgcgccc | ccctcgcggg | cccagctgca  | actgcacttg | cccgccaacc  | 240  |
| ggttgccaggc | ggtggaggga | ggggaagtgg | tgcttccagc  | gtggtacacc | ttgcacgggg  | 300  |
| aggtgtcttc  | atcccagcca | tgggaggtgc | ccttttgtgat | gtggttcttc | aaacagaaaag | 360  |
| aaaaggagga  | tcaggtgttg | tctacatca  | atggggtcac  | aacaagcaaa | cctggagtat  | 420  |
| ccttggtcta  | ctccatgccc | tcccgaacc  | tgctccctcg  | gctggagggt | ctccaggaga  | 480  |
| aagactcttg  | cccctacagc | tgctcggta  | atgtgcaag   | caaacaggc  | aaatctaggg  | 540  |
| gccacagcat  | caaaacctta | gaactcaatg | tactggttcc  | tccagctcct | ccatcctgcc  | 600  |
| gtctccaggg  | tgtgccccat | gtgggggcaa | acgtgacct   | gagctgccag | tctccaagga  | 660  |
| gtaagccgc   | tgtccaatac | cagtgggatc | ggcagcttcc  | atccttccag | actttctttg  | 720  |
| caccagcatt  | agatgtcatc | cgtgggtctt | taagcctcac  | caacctttcg | tcttccatgg  | 780  |
| ctggagtcta  | tgtctgcaag | gccacaatg  | aggtgggcac  | tgcccaatgt | aatgtgacgc  | 840  |
| tggaaagtgag | cacaggccct | ggagctgcag | tggttgctgg  | agctgttgtg | ggtacctctg  | 900  |
| ttggactggg  | gttgctggct | gggctggtcc | tcttgtagca  | ccgcgggggc | aaggccctgg  | 960  |
| aggagccagc  | caatgatata | aaggaggatg | ccattgctcc  | ccggaccctg | ccctggccca  | 1020 |
| agagctcaga  | cacaatctcc | aagaatggga | ccctttctct  | tgtcacctcc | gcacgagccc  | 1080 |
| tccggccacc  | ccatggccct | cccaggcctc | gtgcattgac  | ccccagccc  | agtccttcca  | 1140 |
| gccaggccct  | gcctcaccct | agactgccca | cgacagatgg  | ggccacccc  | caaccaatat  | 1200 |
| cccccatccc  | tgggtggggt | tcttctctct | gcttgagccg  | catgggtgct | gtgctgtgta  | 1260 |
| tggtgccctgc | ccagagtcaa | gctggctctc | tggatatgat  | accccaccac | tcattggcta  | 1320 |
| aaggatttg   | ggtctctcct | tctataaagg | gtcacctcta  | gcacagaggc | ctgagtcatg  | 1380 |
| ggaaagagtc  | acactcctga | cccttagtac | tctgccccca  | cctctcttta | ctgtgggaaa  | 1440 |
| accatctcag  | taagacctaa | gtgtccagga | gacagaagga  | gaagaggaag | tggatctgga  | 1500 |
| attgggagga  | gcctccaccc | accctgact  | cctccttatg  | aagccagctg | ctgaaattag  | 1560 |
| ctactcacca  | agagtgaggg | gcagagactt | ccagtcactg  | agtctcccag | gcccccttga  | 1620 |
| tctgtacccc  | accctatatc | aacaccaccc | ttggtcccca  | ctccagctcc | ctgtattgat  | 1680 |
| ataaactgtc  | aggctggctt | ggttaggttt | tactggggca  | gaggataggg | aatctcttat  | 1740 |
| taaaactaac  | atgaaatatg | tgttgttttc | atttgcaaat  | ttaaataaag | atacataatg  | 1800 |
| tttqtatgaa  | aaa        |            |             |            |             | 1813 |

<211> 390

<213> Home

Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe Leu

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
| 1   |     |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |  |  |  |  |
| Phe | Leu | Gly | Leu | Ser | Ala | Leu | Ala | Pro | Pro | Ser | Arg | Ala | Gln | Leu | Gln |  |  |  |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |  |  |
| Leu | His | Leu | Pro | Ala | Asn | Arg | Leu | Gln | Ala | Val | Glu | Gly | Gly | Glu | Val |  |  |  |  |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |  |  |  |  |
| Val | Leu | Pro | Ala | Trp | Tyr | Thr | Leu | His | Gly | Glu | Val | Ser | Ser | Ser | Gln |  |  |  |  |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |  |  |  |  |
| Pro | Trp | Glu | Val | Pro | Phe | Val | Met | Trp | Phe | Phe | Lys | Gln | Lys | Glu | Lys |  |  |  |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |  |  |  |
| Glu | Asp | Gln | Val | Leu | Ser | Tyr | Ile | Asn | Gly | Val | Thr | Thr | Ser | Lys | Pro |  |  |  |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |  |  |  |
| Gly | Val | Ser | Leu | Val | Tyr | Ser | Met | Pro | Ser | Arg | Asn | Leu | Ser | Leu | Arg |  |  |  |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |  |  |
| Leu | Glu | Gly | Leu | Gln | Glu | Lys | Asp | Ser | Gly | Pro | Tyr | Ser | Cys | Ser | Val |  |  |  |  |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |  |  |  |  |
| Asn | Val | Gln | Asp | Lys | Gln | Gly | Lys | Ser | Arg | Gly | His | Ser | Ile | Lys | Thr |  |  |  |  |
|     |     |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |  |  |  |  |
| Leu | Glu | Leu | Asn | Val | Leu | Val | Pro | Pro | Ala | Pro | Pro | Ser | Cys | Arg | Leu |  |  |  |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |  |  |  |
| Gln | Gly | Val | Pro | His | Val | Gly | Ala | Asn | Val | Thr | Leu | Ser | Cys | Gln | Ser |  |  |  |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |  |  |  |  |
| Pro | Arg | Ser | Lys | Pro | Ala | Val | Gln | Tyr | Gln | Trp | Asp | Arg | Gln | Leu | Pro |  |  |  |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |  |  |  |
| Ser | Phe | Gln | Thr | Phe | Phe | Ala | Pro | Ala | Leu | Asp | Val | Ile | Arg | Gly | Ser |  |  |  |  |
|     |     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |  |  |  |  |
| Leu | Ser | Leu | Thr | Asn | Leu | Ser | Ser | Ser | Met | Ala | Gly | Val | Tyr | Val | Cys |  |  |  |  |
|     |     |     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |  |  |  |  |
| Lys | Ala | His | Asn | Glu | Val | Gly | Thr | Ala | Gln | Cys | Asn | Val | Thr | Leu | Glu |  |  |  |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |  |  |  |
| Val | Ser | Thr | Gly | Pro | Gly | Ala | Ala | Val | Val | Ala | Gly | Ala | Val | Val | Gly |  |  |  |  |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |  |  |  |  |
| Thr | Leu | Val | Gly | Leu | Gly | Leu | Leu | Ala | Gly | Leu | Val | Leu | Leu | Tyr | His |  |  |  |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |  |  |  |
| Arg | Arg | Gly | Lys | Ala | Leu | Glu | Glu | Pro | Ala | Asn | Asp | Ile | Lys | Glu | Asp |  |  |  |  |
|     |     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |  |  |  |  |

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 42  
 ggccacagca tcaaaacctt agaactcaat gtactgggtc ctccagctcc 50  
  
 <210> 43  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 43  
 gtgtgacaca gcgtgggc 18  
  
 <210> 44  
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 <212> DNA  
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 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 44  
 gaccggcagg cttctgcg 18  
  
 <210> 45  
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 <212> DNA  
 <213> Artificial Sequence  
  
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 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 45  
 cagcagcttc agccaccagg agtgg 25  
  
 <210> 46  
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 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 46  
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 <210> 47

090506-0704  
 T04120-9905060



<211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 47  
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<210> 48  
 <211> 2822  
 <212> DNA  
 <213> Homo sapiens

<400> 48  
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 gtgaaatacg caatggaatt gaagcctgct attgcaacat gggattttca ggaaatgggt 180  
 tcacaatttg tgaagatgat aatgaatgtg gaaatttaac tcagtcctgt ggcgaaaatg 240  
 ctaattgcac taacacagaa ggaagttatt attgtatgtg tgtacctggc ttcagatcca 300  
 gcagtaacca agacaggttt atcactaatg atggaaccgt ctgtatagaa aatgtgaatg 360  
 caaactgcc a ttagataat gtctgtatag ctgcaaatat taataaaaact ttaacaaaaa 420  
 tcagatccat aaaagaacct gtggctttgc tacaagaagt ctatagaaat tctgtgacag 480  
 atctttcacc aacagatata attacatata tagaaatatt agctgaatca tcttcattac 540  
 taggttacaa gaacaacact atctcagcca aggacaccct ttctaactca actcttactg 600  
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 atgctttcca ggggatgttc atttttttat tctgtgtgtg tttatctaga aagattcaag 2040  
 aagaatatta cagattgttc aaaaatgtcc cctgttgttt tggatgttta aggtaaacat 2100  
 agagaatggt ggataattac aactgcacaa aaataaaaat tccaagctgt ggatgaccaa 2160

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aa

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<210> 49
<211> 690
<212> PRT
<213> Homo sapiens

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Ser Tyr Thr Gln Asn Cys Thr Lys Thr Pro Cys Leu Pro Asn Ala Lys
      20              25              30

Cys Glu Ile Arg Asn Gly Ile Glu Ala Cys Tyr Cys Asn Met Gly Phe
      35              40              45

Ser Gly Asn Gly Val Thr Ile Cys Glu Asp Asp Asn Glu Cys Gly Asn
      50              55              60

Leu Thr Gln Ser Cys Gly Glu Asn Ala Asn Cys Thr Asn Thr Glu Gly
      65              70              75              80

Ser Tyr Tyr Cys Met Cys Val Pro Gly Phe Arg Ser Ser Ser Asn Gln
      85              90              95

Asp Arg Phe Ile Thr Asn Asp Gly Thr Val Cys Ile Glu Asn Val Asn
      100             105             110

Ala Asn Cys His Leu Asp Asn Val Cys Ile Ala Ala Asn Ile Asn Lys
      115             120             125

Thr Leu Thr Lys Ile Arg Ser Ile Lys Glu Pro Val Ala Leu Leu Gln
      130             135             140

Glu Val Tyr Arg Asn Ser Val Thr Asp Leu Ser Pro Thr Asp Ile Ile
      145             150             155             160

Thr Tyr Ile Glu Ile Leu Ala Glu Ser Ser Ser Leu Leu Gly Tyr Lys
      165             170             175

Asn Asn Thr Ile Ser Ala Lys Asp Thr Leu Ser Asn Ser Thr Leu Thr

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|   |     |     |     |     |     |
|---|-----|-----|-----|-----|-----|
|   | 180 |     | 185 |     | 190 |
| Glu Phe Val Lys Thr Val Asn Asn Phe Val Gln Arg Asp Thr Phe Val | 195 | 200 | 205 |     |     |
| Val Trp Asp Lys Leu Ser Val Asn His Arg Arg Thr His Leu Thr Lys | 210 | 215 | 220 |     |     |
| Leu Met His Thr Val Glu Gln Ala Thr Leu Arg Ile Ser Gln Ser Phe | 225 | 230 | 235 | 240 |     |
| Gln Lys Thr Thr Glu Phe Asp Thr Asn Ser Thr Asp Ile Ala Leu Lys | 245 | 250 | 255 |     |     |
| Val Phe Phe Phe Asp Ser Tyr Asn Met Lys His Ile His Pro His Met | 260 | 265 | 270 |     |     |
| Asn Met Asp Gly Asp Tyr Ile Asn Ile Phe Pro Lys Arg Lys Ala Ala | 275 | 280 | 285 |     |     |
| Tyr Asp Ser Asn Gly Asn Val Ala Val Ala Phe Leu Tyr Tyr Lys Ser | 290 | 295 | 300 |     |     |
| Ile Gly Pro Leu Leu Ser Ser Ser Asp Asn Phe Leu Leu Lys Pro Gln | 305 | 310 | 315 | 320 |     |
| Asn Tyr Asp Asn Ser Glu Glu Glu Glu Arg Val Ile Ser Ser Val Ile | 325 | 330 | 335 |     |     |
| Ser Val Ser Met Ser Ser Asn Pro Pro Thr Leu Tyr Glu Leu Glu Lys | 340 | 345 | 350 |     |     |
| Ile Thr Phe Thr Leu Ser His Arg Lys Val Thr Asp Arg Tyr Arg Ser | 355 | 360 | 365 |     |     |
| Leu Cys Ala Phe Trp Asn Tyr Ser Pro Asp Thr Met Asn Gly Ser Trp | 370 | 375 | 380 |     |     |
| Ser Ser Glu Gly Cys Glu Leu Thr Tyr Ser Asn Glu Thr His Thr Ser | 385 | 390 | 395 | 400 |     |
| Cys Arg Cys Asn His Leu Thr His Phe Ala Ile Leu Met Ser Ser Gly | 405 | 410 | 415 |     |     |
| Pro Ser Ile Gly Ile Lys Asp Tyr Asn Ile Leu Thr Arg Ile Thr Gln | 420 | 425 | 430 |     |     |
| Leu Gly Ile Ile Ile Ser Leu Ile Cys Leu Ala Ile Cys Ile Phe Thr | 435 | 440 | 445 |     |     |
| Phe Trp Phe Phe Ser Glu Ile Gln Ser Thr Arg Thr Thr Ile His Lys | 450 | 455 | 460 |     |     |

<222> (61)

<223> a, t, c or g

<400> 50

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gtattgggtcc ctttgctttc atcatctgac aacttcttat tgaaacctca aaattatgat 180
aattctgaag aggaggaaa agtcatatct tcagtaattt cagtctcaat gagctcaaac 240
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gataggtata ggagtctatg tggcattttg gaatactcac ctgataccat gaatggcagc 360
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tataatattc ttacaaggat cactcaacta ggaataatta ttccactgat ttgtcttgcc 540
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<210> 51

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 51

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<210> 52

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 52

ggagtagaaa gcgcatgg 18

<210> 53

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 53

cacctgatac catgaatggc ag 22

<210> 54

<211> 18

<212> DNA

T03T03: 99090909

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 54

cgagctcgaa ttaattcg

18

<210> 55

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 55

ggatctcctg agctcagg

18

<210> 56

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 56

cctagttgag tgatccttgt aag

23

<210> 57

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 57

atgagacca cacctcatgc cgctgtaatc acctgacaca ttttgcaatt

50

<210> 58

<211> 2137

<212> DNA

<213> Homo sapiens

<400> 58

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09505050-0404

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<210> 59

<211> 216

<212> PRT

<213> Homo sapiens

<400> 59

Met Arg Ser Gly Cys Val Val Val His Val Trp Ile Leu Ala Gly Leu  
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Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala Gly Pro  
 20 25 30

His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg His Leu Tyr  
 35 40 45

Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala  
 50 55 60

Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser Ala His Ser Leu Leu  
 65 70 75 80  
 Glu Ile Lys Ala Val Ala Leu Arg Thr Val Ala Ile Lys Gly Val His  
 85 90 95  
 Ser Val Arg Tyr Leu Cys Met Gly Ala Asp Gly Lys Met Gln Gly Leu  
 100 105 110  
 Leu Gln Tyr Ser Glu Glu Asp Cys Ala Phe Glu Glu Glu Ile Arg Pro  
 115 120 125  
 Asp Gly Tyr Asn Val Tyr Arg Ser Glu Lys His Arg Leu Pro Val Ser  
 130 135 140  
 Leu Ser Ser Ala Lys Gln Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu  
 145 150 155 160  
 Pro Leu Ser His Phe Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro  
 165 170 175  
 Glu Asp Leu Arg Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu  
 180 185 190  
 Glu Thr Asp Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala  
 195 200 205  
 Val Arg Ser Pro Ser Phe Glu Lys  
 210 215

<210> 60

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 60

atccgcccag atggctacaa tgtgta

26

<210> 61

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 61

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42



<210> 62  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 62  
 ccagtcggt gacaagccca aa

22

<210> 63  
 <211> 1295  
 <212> DNA  
 <213> Homo sapiens

<400> 63  
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 aaccccaaag aagactgttt cctccagatt agagtggaag aaactgggtc ggagtgtctc 300  
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<210> 64  
 <211> 312  
 <212> PRT  
 <213> Homo sapiens

<400> 64  
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 Leu Val Val Ala Leu Gly Tyr His Lys Ala Tyr Gly Phe Ser Ala Pro  
 20 25 30

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Lys Asp Gln Gln Val Val Thr Ala Val Glu Tyr Gln Glu Ala Ile Leu  
           35                                  40                                  45  
 Ala Cys Lys Thr Pro Lys Lys Thr Val Ser Ser Arg Leu Glu Trp Lys  
           50                                  55                                  60  
 Lys Leu Gly Arg Ser Val Ser Phe Val Tyr Tyr Gln Gln Thr Leu Gln  
           65                                  70                                  75                                  80  
 Gly Asp Phe Lys Asn Arg Ala Glu Met Ile Asp Phe Asn Ile Arg Ile  
                                   85                                  90                                  95  
 Lys Asn Val Thr Arg Ser Asp Ala Gly Lys Tyr Arg Cys Glu Val Ser  
                                   100                                  105                                  110  
 Ala Pro Ser Glu Gln Gly Gln Asn Leu Glu Glu Asp Thr Val Thr Leu  
                                   115                                  120                                  125  
 Glu Val Leu Val Ala Pro Ala Val Pro Ser Cys Glu Val Pro Ser Ser  
           130                                  135                                  140  
 Ala Leu Ser Gly Thr Val Val Glu Leu Arg Cys Gln Asp Lys Glu Gly  
           145                                  150                                  155                                  160  
 Asn Pro Ala Pro Glu Tyr Thr Trp Phe Lys Asp Gly Ile Arg Leu Leu  
                                   165                                  170                                  175  
 Glu Asn Pro Arg Leu Gly Ser Gln Ser Thr Asn Ser Ser Tyr Thr Met  
                                   180                                  185                                  190  
 Asn Thr Lys Thr Gly Thr Leu Gln Phe Asn Thr Val Ser Lys Leu Asp  
                                   195                                  200                                  205  
 Thr Gly Glu Tyr Ser Cys Glu Ala Arg Asn Ser Val Gly Tyr Arg Arg  
           210                                  215                                  220  
 Cys Pro Gly Lys Arg Met Gln Val Asp Asp Leu Asn Ile Ser Gly Ile  
           225                                  230                                  235                                  240  
 Ile Ala Ala Val Val Val Val Ala Leu Val Ile Ser Val Cys Gly Leu  
                                   245                                  250                                  255  
 Gly Val Cys Tyr Ala Gln Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser  
                                   260                                  265                                  270  
 Phe Gln Lys Ser Asn Ser Ser Ser Lys Ala Thr Thr Met Ser Glu Asn  
                                   275                                  280                                  285  
 Val Gln Trp Leu Thr Pro Val Ile Pro Ala Leu Trp Lys Ala Ala Ala  
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 Gly Gly Ser Arg Gly Gln Glu Phe

305 310

<210> 65  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 65  
 atcgttgtga agttagtgcc cc 22

<210> 66  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 66  
 acctgcgata tccaacagaa ttg 23

<210> 67  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 67  
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<210> 68  
 <211> 2639  
 <212> DNA  
 <213> Homo sapiens

<400> 68  
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 gcatcatgct gctattcctg caaatactga agaagcatgg gatttaaata ttttacttct 180  
 aaataaatga attactcaat ctcctatgac catctataca tactccacct tcaaaaagta 240  
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<210> 69

<211> 708

<212> PRT

<213> Homo sapiens

<400> 69

Met Lys Asp Met Pro Leu Arg Ile His Val Leu Leu Gly Leu Ala Ile  
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Thr Thr Leu Val Gln Ala Val Asp Lys Lys Val Asp Cys Pro Arg Leu  
20 25 30

Cys Thr Cys Glu Ile Arg Pro Trp Phe Thr Pro Arg Ser Ile Tyr Met  
35 40 45

Glu Ala Ser Thr Val Asp Cys Asn Asp Leu Gly Leu Leu Thr Phe Pro  
50 55 60



|  |     |     |
|--|-----|-----|
| 340  | 345 | 350 |
| Thr Ile Glu Ser Leu Pro Asn Leu Lys Glu Ile Ser Ile His Ser Asn<br>355 360 365     |     |     |
| Pro Ile Arg Cys Asp Cys Val Ile Arg Trp Met Asn Met Asn Lys Thr<br>370 375 380     |     |     |
| Asn Ile Arg Phe Met Glu Pro Asp Ser Leu Phe Cys Val Asp Pro Pro<br>385 390 395 400 |     |     |
| Glu Phe Gln Gly Gln Asn Val Arg Gln Val His Phe Arg Asp Met Met<br>405 410 415     |     |     |
| Glu Ile Cys Leu Pro Leu Ile Ala Pro Glu Ser Phe Pro Ser Asn Leu<br>420 425 430     |     |     |
| Asn Val Glu Ala Gly Ser Tyr Val Ser Phe His Cys Arg Ala Thr Ala<br>435 440 445     |     |     |
| Glu Pro Gln Pro Glu Ile Tyr Trp Ile Thr Pro Ser Gly Gln Lys Leu<br>450 455 460     |     |     |
| Leu Pro Asn Thr Leu Thr Asp Lys Phe Tyr Val His Ser Glu Gly Thr<br>465 470 475 480 |     |     |
| Leu Asp Ile Asn Gly Val Thr Pro Lys Glu Gly Gly Leu Tyr Thr Cys<br>485 490 495     |     |     |
| Ile Ala Thr Asn Leu Val Gly Ala Asp Leu Lys Ser Val Met Ile Lys<br>500 505 510     |     |     |
| Val Asp Gly Ser Phe Pro Gln Asp Asn Asn Gly Ser Leu Asn Ile Lys<br>515 520 525     |     |     |
| Ile Arg Asp Ile Gln Ala Asn Ser Val Leu Val Ser Trp Lys Ala Ser<br>530 535 540     |     |     |
| Ser Lys Ile Leu Lys Ser Ser Val Lys Trp Thr Ala Phe Val Lys Thr<br>545 550 555 560 |     |     |
| Glu Asn Ser His Ala Ala Gln Ser Ala Arg Ile Pro Ser Asp Val Lys<br>565 570 575     |     |     |
| Val Tyr Asn Leu Thr His Leu Asn Pro Ser Thr Glu Tyr Lys Ile Cys<br>580 585 590     |     |     |
| Ile Asp Ile Pro Thr Ile Tyr Gln Lys Asn Arg Lys Lys Cys Val Asn<br>595 600 605     |     |     |
| Val Thr Thr Lys Gly Leu His Pro Asp Gln Lys Glu Tyr Glu Lys Asn<br>610 615 620     |     |     |

29

|   |             |
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| Asn Thr Thr Thr Leu Met Ala Cys Leu Gly Gly Leu Leu Gly Ile Ile |             |
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| Gly Val Ile Cys Leu Ile Ser Cys Leu Ser Pro Glu Met Asn Cys Asp |             |
|   | 645 650 655 |
| Gly Gly His Ser Tyr Val Arg Asn Tyr Leu Gln Lys Pro Thr Phe Ala |             |
|   | 660 665 670 |
| Leu Gly Glu Leu Tyr Pro Pro Leu Ile Asn Leu Trp Glu Ala Gly Lys |             |
|   | 675 680 685 |
| Glu Lys Ser Thr Ser Leu Lys Val Lys Ala Thr Val Ile Gly Leu Pro |             |
|   | 690 695 700 |
| Thr Asn Met Ser   |             |
| 705   |             |

<210> 70  
 <211> 1305  
 <212> DNA  
 <213> Homo sapiens

<400> 70

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| agctgcagcc  | ttttgaaaca | cgcaagaagg  | aaatcaatag | tgtggacagg | gctggaacct | 120  |
| ttaccacgct  | tggttgagta | gatgaggaat  | gggctcgtga | ttatgctgac | attccagcat | 180  |
| gaatctggta  | gacctgtggt | taaccggttc  | cctctccatg | tgtctcctcc | tacaaagttt | 240  |
| tgttcttatg  | atactgtgct | ttcattctgc  | cagtatgtgt | cccaagggtc | gtctttgttc | 300  |
| ttcctctggg  | ggttttaaag | tcacctgtag  | caatgcaaag | ctcaaggaaa | tacctagaga | 360  |
| tcttctcctc  | gaaacagtct | tactgtatct  | ggactccaat | cagatcacat | ctattcccaa | 420  |
| tgaaatTTTT  | aaggacctcc | atcaactgag  | agttctcaac | ctgtccaaaa | atggcattga | 480  |
| gtttatcgat  | gagcatgcct | tcaaaggagt  | agctgaaacc | ttgcagactc | tggacttgtc | 540  |
| cgacaatcgg  | attcaaagtg | tgcacaaaaa  | tgccttcaat | aacctgaagg | ccagggccag | 600  |
| aattgccaac  | aacccctggc | actgcgactg  | tactctacag | caagttctga | ggagcatggc | 660  |
| gtccaatcat  | gagacagccc | acaacgtgat  | ctgtaaaacg | tccgtgttgg | atgaacatgc | 720  |
| tggcagacca  | ttcctcaatg | ctgccaacga  | cgctgacctt | tgtaacctcc | ctaaaaaaac | 780  |
| taccgattat  | gccatgctgg | tcaccatggt  | tggctgggtc | actatggtga | tctcatatgt | 840  |
| ggtatattat  | gtgaggcaaa | atcaggagga  | tgcccggaga | cacctcgaat | acttgaaatc | 900  |
| cctgccaaagc | aggcagaaga | aagcagatga  | acctgatgat | attagcactg | tggatatagt | 960  |
| tccaaactga  | ctgtcattga | gaaagaaaaga | aagtagtttg | cgattgcagt | agaaataagt | 1020 |
| ggtttacttc  | tcccatccat | tgtaaacatt  | tgaaactttg | tatttcagtt | ttttttgaat | 1080 |
| tatgccactg  | ctgaactttt | aacaaacact  | acaacataaa | taatttgagt | ttaggtgatc | 1140 |
| caccctttaa  | ttgtaccccc | gatggtatat  | ttctgagtaa | gctactatct | gaacattagt | 1200 |
| tagatccatc  | tcactattta | ataatgaaat  | ttattttttt | aattttaaag | caaataaaag | 1260 |
| cttaactttg  | aaccatggga | aaaaaaaaaa  | aaaaaaaaaa | aaaca      |            | 1305 |

<210> 71  
 <211> 259  
 <212> PRT  
 <213> Homo sapiens

<400> 71





&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 72

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&lt;210&gt; 73

&lt;211&gt; 620

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 73

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1 5 10 15

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Ser Met Leu His Glu Leu Leu Arg Leu Gln Glu Ile Gln Leu Val Gly  
 305 310 315 320  
 Gly Gln Leu Ala Val Val Glu Pro Tyr Ala Phe Arg Gly Leu Asn Tyr  
 325 330 335  
 Leu Arg Val Leu Asn Val Ser Gly Asn Gln Leu Thr Thr Leu Glu Glu  
 340 345 350  
 Ser Val Phe His Ser Val Gly Asn Leu Glu Thr Leu Ile Leu Asp Ser  
 355 360 365  
 Asn Pro Leu Ala Cys Asp Cys Arg Leu Leu Trp Val Phe Arg Arg Arg  
 370 375 380  
 Trp Arg Leu Asn Phe Asn Arg Gln Gln Pro Thr Cys Ala Thr Pro Glu  
 385 390 395 400  
 Phe Val Gln Gly Lys Glu Phe Lys Asp Phe Pro Asp Val Leu Leu Pro  
 405 410 415  
 Asn Tyr Phe Thr Cys Arg Arg Ala Arg Ile Arg Asp Arg Lys Ala Gln  
 420 425 430  
 Gln Val Phe Val Asp Glu Gly His Thr Val Gln Phe Val Cys Arg Ala  
 435 440 445  
 Asp Gly Asp Pro Pro Pro Ala Ile Leu Trp Leu Ser Pro Arg Lys His  
 450 455 460  
 Leu Val Ser Ala Lys Ser Asn Gly Arg Leu Thr Val Phe Pro Asp Gly  
 465 470 475 480  
 Thr Leu Glu Val Arg Tyr Ala Gln Val Gln Asp Asn Gly Thr Tyr Leu  
 485 490 495  
 Cys Ile Ala Ala Asn Ala Gly Gly Asn Asp Ser Met Pro Ala His Leu  
 500 505 510  
 His Val Arg Ser Tyr Ser Pro Asp Trp Pro His Gln Pro Asn Lys Thr  
 515 520 525  
 Phe Ala Phe Ile Ser Asn Gln Pro Gly Glu Gly Glu Ala Asn Ser Thr  
 530 535 540  
 Arg Ala Thr Val Pro Phe Pro Phe Asp Ile Lys Thr Leu Ile Ile Ala  
 545 550 555 560  
 Thr Thr Met Gly Phe Ile Ser Phe Leu Gly Val Val Leu Phe Cys Leu  
 565 570 575  
 Val Leu Leu Phe Leu Trp Ser Arg Gly Lys Gly Asn Thr Lys His Asn

| 580  | 585 | 590 |    |
|--|-----|-----|----|
| Ile Glu Ile Glu Tyr Val Pro Arg Lys Ser Asp Ala Gly Ile Ser Ser              |     |     |    |
| 595  | 600 | 605 |    |
| Ala Asp Ala Pro Arg Lys Phe Asn Met Lys Met Ile                              |     |     |    |
| 610  | 615 | 620 |    |
| <210> 74   |     |     |    |
| <211> 22   |     |     |    |
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| <223> Description of Artificial Sequence: Synthetic<br>oligonucleotide probe |     |     |    |
| <400> 74   |     |     |    |
| tcacctggag cctttattgg cc   |     |     | 22 |
| <210> 75   |     |     |    |
| <211> 23   |     |     |    |
| <212> DNA  |     |     |    |
| <213> Artificial Sequence  |     |     |    |
| <220>  |     |     |    |
| <223> Description of Artificial Sequence: Synthetic<br>oligonucleotide probe |     |     |    |
| <400> 75   |     |     |    |
| ataccagcta taaccaggct gcg  |     |     | 23 |
| <210> 76   |     |     |    |
| <211> 52   |     |     |    |
| <212> DNA  |     |     |    |
| <213> Artificial Sequence  |     |     |    |
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| <223> Description of Artificial Sequence: Synthetic<br>oligonucleotide probe |     |     |    |
| <400> 76   |     |     |    |
| caacagtaag tggtttgatg ctcttccaaa tctagagatt ctgatgattg                       |     |     | 50 |
| gg   |     |     | 52 |
| <210> 77   |     |     |    |
| <211> 22   |     |     |    |
| <212> DNA  |     |     |    |
| <213> Artificial Sequence  |     |     |    |
| <220>  |     |     |    |
| <223> Description of Artificial Sequence: Synthetic<br>oligonucleotide probe |     |     |    |

<400> 77  
 ccatgtgtct cctcctacaa ag 22

<210> 78  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 78  
 gggaatagat gtgatctgat tgg 23

<210> 79  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 79  
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<210> 80  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 80  
 agcaaccgcc tgaagctcat cc 22

<210> 81  
 <211> 24  
 <212> DNA  
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<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 81  
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<210> 82

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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<210> 83
<211> 1685
<212> DNA
<213> Homo sapiens
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<210> 84
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<212> PRT
<213> Homo sapiens
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<400> 84

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 Pro Trp Thr Ser Asp Glu Thr Val Val Ala Gly Gly Thr Val Val Leu  
 35 40 45  
 Lys Cys Gln Val Lys Asp His Glu Asp Ser Ser Leu Gln Trp Ser Asn  
 50 55 60  
 Pro Ala Gln Gln Thr Leu Tyr Phe Gly Glu Lys Arg Ala Leu Arg Asp  
 65 70 75 80  
 Asn Arg Ile Gln Leu Val Thr Ser Thr Pro His Glu Leu Ser Ile Ser  
 85 90 95  
 Ile Ser Asn Val Ala Leu Ala Asp Glu Gly Glu Tyr Thr Cys Ser Ile  
 100 105 110  
 Phe Thr Met Pro Val Arg Thr Ala Lys Ser Leu Val Thr Val Leu Gly  
 115 120 125  
 Ile Pro Gln Lys Pro Ile Ile Thr Gly Tyr Lys Ser Ser Leu Arg Glu  
 130 135 140  
 Lys Asp Thr Ala Thr Leu Asn Cys Gln Ser Ser Gly Ser Lys Pro Ala  
 145 150 155 160  
 Ala Arg Leu Thr Trp Arg Lys Gly Asp Gln Glu Leu His Gly Glu Pro  
 165 170 175  
 Thr Arg Ile Gln Glu Asp Pro Asn Gly Lys Thr Phe Thr Val Ser Ser  
 180 185 190  
 Ser Val Thr Phe Gln Val Thr Arg Glu Asp Asp Gly Ala Ser Ile Val  
 195 200 205  
 Cys Ser Val Asn His Glu Ser Leu Lys Gly Ala Asp Arg Ser Thr Ser  
 210 215 220  
 Gln Arg Ile Glu Val Leu Tyr Thr Pro Thr Ala Met Ile Arg Pro Asp  
 225 230 235 240  
 Pro Pro His Pro Arg Glu Gly Gln Lys Leu Leu Leu His Cys Glu Gly  
 245 250 255  
 Arg Gly Asn Pro Val Pro Gln Gln Tyr Leu Trp Glu Lys Glu Gly Ser  
 260 265 270  
 Val Pro Pro Leu Lys Met Thr Gln Glu Ser Ala Leu Ile Phe Pro Phe  
 275 280 285

Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr Ser Asn  
 290 295 300

Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu Asn Val Asn Asp Pro Ser  
 305 310 315 320

Pro Val Pro Ser Ser Ser Ser Thr Tyr His Ala Ile Ile Gly Gly Ile  
 325 330 335

Val Ala Phe Ile Val Phe Leu Leu Leu Ile Met Leu Ile Phe Leu Gly  
 340 345 350

His Tyr Leu Ile Arg His Lys Gly Thr Tyr Leu Thr His Glu Ala Lys  
 355 360 365

Gly Ser Asp Asp Ala Pro Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu  
 370 375 380

Gly Gly Gln Ser Gly Gly Asp Asp Lys Lys Glu Tyr Phe Ile  
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<210> 85

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 85

gctaggaatt ccacagaagc cc

22

<210> 86

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 86

aacctggaat gtcaccgagc tg

22

<210> 87

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

09505056 07204



<400> 87  
cctagcacag tgacgagggg cttggc 26

<220>  
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oligonucleotide probe

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<210> 89
<211> 50
<212> DNA
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<400> 89  
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| ggcttcggac  | attggagcac | taaatagaact | tgaatttgtgt | ctgtggcgag | caggatgggtc   | 120  |  |
| gctgttactt  | tgtgatgaga | tcgggggatga | attgctcgct  | ttaaaaatgc | tgctttggat    | 180  |  |
| tctgttgctg  | gagacgtctc | tttgttttgc  | cgctggaaac  | gttacagggg | acgtttgcaa    | 240  |  |
| agagaagatc  | tgttcctgca | atgagataga  | agggggacct  | cacgtagact | gtgaaaaaaa    | 300  |  |
| gggcttcaca  | agtctgcagc | gtttcactgc  | cccgacttcc  | cagttttacc | at ttat tttct | 360  |  |
| gcatggcaat  | tcctcactc  | gacttttccc  | taatgagttc  | gctaactttt | ataatgcggt    | 420  |  |
| tagtttgcac  | atggaaaaca | atggcttgca  | tgaaatcggt  | ccgggggctt | ttctggggct    | 480  |  |
| gcagctggtg  | aaaaggctgc | acatcaacaa  | caacaagatc  | aagtcctttc | gaaagcagac    | 540  |  |
| ttttctgggg  | ctggacgatc | tggaaatatct | ccaggctgat  | tttaatttat | tacgagatat    | 600  |  |
| agacccgggg  | gccttcagg  | acttgaacaa  | gctggagggtg | ctcattttaa | atgacaatct    | 660  |  |
| catcagcacc  | ctacctgcca | acgtgttcca  | gtatgtgccc  | atcaccaccc | tcgacctccg    | 720  |  |
| gggtaacagg  | ctgaaaacgc | tgccttatga  | ggaggctctg  | gagcaaatcc | ctggatttgc    | 780  |  |
| ggagatcctg  | ctagaggata | acccttgggg  | ctgcacctgt  | gatctgctct | ccctgaaaga    | 840  |  |
| atggctggaa  | aacattccca | agaatgcctt  | gatcggcoga  | gtggtctgcg | aagccccac     | 900  |  |
| cagactgcag  | ggtaaagacc | tcaatgaaac  | caccgaacag  | gacttgtgtc | ctttgaaaaa    | 960  |  |
| ccgagtggat  | tctagtctcc | cggcgcccc   | tgcccaagaa  | gagacctttg | ctcctggacc    | 1020 |  |
| cctgccaaact | cctttcaaga | caaattgggca | agaggatcat  | gccacaccag | ggctctgctcc   | 1080 |  |

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<211> 696

<212> PRT

<213> Homo sapiens

<400> 91

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Gly Asn Val Thr Gly Asp Val Cys Lys Glu Lys Ile Cys Ser Cys Asn  
 20 25 30

Glu Ile Glu Gly Asp Leu His Val Asp Cys Glu Lys Lys Gly Phe Thr  
 35 40 45

Ser Leu Gln Arg Phe Thr Ala Pro Thr Ser Gln Phe Tyr His Leu Phe  
 50 55 60

Leu His Gly Asn Ser Leu Thr Arg Leu Phe Pro Asn Glu Phe Ala Asn  
 65 70 75 80

Phe Tyr Asn Ala Val Ser Leu His Met Glu Asn Asn Gly Leu His Glu  
 85 90 95

Ile Val Pro Gly Ala Phe Leu Gly Leu Gln Leu Val Lys Arg Leu His  
 100 105 110  
 Ile Asn Asn Asn Lys Ile Lys Ser Phe Arg Lys Gln Thr Phe Leu Gly  
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 Leu Asp Asp Leu Glu Tyr Leu Gln Ala Asp Phe Asn Leu Leu Arg Asp  
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 145 150 155 160  
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 165 170 175  
 Val Pro Ile Thr His Leu Asp Leu Arg Gly Asn Arg Leu Lys Thr Leu  
 180 185 190  
 Pro Tyr Glu Glu Val Leu Glu Gln Ile Pro Gly Ile Ala Glu Ile Leu  
 195 200 205  
 Leu Glu Asp Asn Pro Trp Asp Cys Thr Cys Asp Leu Leu Ser Leu Lys  
 210 215 220  
 Glu Trp Leu Glu Asn Ile Pro Lys Asn Ala Leu Ile Gly Arg Val Val  
 225 230 235 240  
 Cys Glu Ala Pro Thr Arg Leu Gln Gly Lys Asp Leu Asn Glu Thr Thr  
 245 250 255  
 Glu Gln Asp Leu Cys Pro Leu Lys Asn Arg Val Asp Ser Ser Leu Pro  
 260 265 270  
 Ala Pro Pro Ala Gln Glu Glu Thr Phe Ala Pro Gly Pro Leu Pro Thr  
 275 280 285  
 Pro Phe Lys Thr Asn Gly Gln Glu Asp His Ala Thr Pro Gly Ser Ala  
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 Pro Asn Gly Gly Thr Lys Ile Pro Gly Asn Trp Gln Ile Lys Ile Arg  
 305 310 315 320  
 Pro Thr Ala Ala Ile Ala Thr Gly Ser Ser Arg Asn Lys Pro Leu Ala  
 325 330 335  
 Asn Ser Leu Pro Cys Pro Gly Gly Cys Ser Cys Asp His Ile Pro Gly  
 340 345 350  
 Ser Gly Leu Lys Met Asn Cys Asn Asn Arg Asn Val Ser Ser Leu Ala  
 355 360 365  
 Asp Leu Lys Pro Lys Leu Ser Asn Val Gln Glu Leu Phe Leu Arg Asp  
 370 375 380

09085055 0720  
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Asn Lys Ile His Ser Ile Arg Lys Ser His Phe Val Asp Tyr Lys Asn  
 385 390 395 400  
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 405 410 415  
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 420 425 430  
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 450 455 460  
 Gly Thr Phe Asn Ala Met Pro Lys Leu Arg Ile Leu Ile Leu Asn Asn  
 465 470 475 480  
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 485 490 495  
 Ser Lys Leu Ser Leu His Asn Asn Tyr Phe Met Tyr Leu Pro Val Ala  
 500 505 510  
 Gly Val Leu Asp Gln Leu Thr Ser Ile Ile Gln Ile Asp Leu His Gly  
 515 520 525  
 Asn Pro Trp Glu Cys Ser Cys Thr Ile Val Pro Phe Lys Gln Trp Ala  
 530 535 540  
 Glu Arg Leu Gly Ser Glu Val Leu Met Ser Asp Leu Lys Cys Glu Thr  
 545 550 555 560  
 Pro Val Asn Phe Phe Arg Lys Asp Phe Met Leu Leu Ser Asn Asp Glu  
 565 570 575  
 Ile Cys Pro Gln Leu Tyr Ala Arg Ile Ser Pro Thr Leu Thr Ser His  
 580 585 590  
 Ser Lys Asn Ser Thr Gly Leu Ala Glu Thr Gly Thr His Ser Asn Ser  
 595 600 605  
 Tyr Leu Asp Thr Ser Arg Val Ser Ile Ser Val Leu Val Pro Gly Leu  
 610 615 620  
 Leu Leu Val Phe Val Thr Ser Ala Phe Thr Val Val Gly Met Leu Val  
 625 630 635 640  
 Phe Ile Leu Arg Asn Arg Lys Arg Ser Lys Arg Arg Asp Ala Asn Ser  
 645 650 655  
 Ser Ala Ser Glu Ile Asn Ser Leu Gln Thr Val Cys Asp Ser Ser Tyr

|   |   |     |     |    |
|---|---|-----|-----|----|
|   | 660   | 665 | 670 |    |
| Trp His Asn Gly Pro Tyr Asn Ala Asp Gly Ala His Arg Val Tyr Asp   |   |     |     |    |
|   | 675   | 680 | 685 |    |
| Cys Gly Ser His Ser Leu Ser Asp                                   |   |     |     |    |
|   | 690   | 695 |     |    |
| <hr/>   |   |     |     |    |
| <210>   | 92  |     |     |    |
| <211>   | 22  |     |     |    |
| <212>   | DNA   |     |     |    |
| <213>   | Artificial Sequence                           |     |     |    |
| <220>   |   |     |     |    |
| <223>   | Description of Artificial Sequence: Synthetic |     |     |    |
|   | oligonucleotide probe                         |     |     |    |
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| gttggatctg ggcaacaata ac  |   |     |     | 22 |
| <210>   | 93  |     |     |    |
| <211>   | 24  |     |     |    |
| <212>   | DNA   |     |     |    |
| <213>   | Artificial Sequence                           |     |     |    |
| <220>   |   |     |     |    |
| <223>   | Description of Artificial Sequence: Synthetic |     |     |    |
|   | oligonucleotide probe                         |     |     |    |
| <400>   | 93  |     |     |    |
| attgttgtgc aggctgagtt taag  |   |     |     | 24 |
| <210>   | 94  |     |     |    |
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| <212>   | DNA   |     |     |    |
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| <223>   | Description of Artificial Sequence: Synthetic |     |     |    |
|   | oligonucleotide probe                         |     |     |    |
| <400>   | 94  |     |     |    |
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| <210>   | 95  |     |     |    |
| <211>   | 2226  |     |     |    |
| <212>   | DNA   |     |     |    |
| <213>   | Homo sapiens                                  |     |     |    |
| <400>   | 95  |     |     |    |
| agtgcactgc gtccctgtga cccggcgcca gctgtgttcc tgaccccaga ataactcagg | 60  |     |     |    |
| gctgcaccgg goctggcagc gctccgcaca catttccgtg cgcggcctaa gggaaactgt | 120   |     |     |    |
| tqqccqctgg gcccgcgggg ggattcttgg cagttggggg gtccgtcggg agcgagggcg | 180   |     |     |    |

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<210> 96

<211> 490

<212> PRT

<213> Homo sapiens

<400> 96

Met Arg Pro Ala Phe Ala Leu Cys Leu Leu Trp Gln Ala Leu Trp Pro  
 1 5 10 15

Gly Pro Gly Gly Gly Glu His Pro Thr Ala Asp Arg Ala Gly Cys Ser  
 20 25 30

Ala Ser Gly Ala Cys Tyr Ser Leu His His Ala Thr Met Lys Arg Gln  
 35 40 45

Ala Ala Glu Glu Ala Cys Ile Leu Arg Gly Gly Ala Leu Ser Thr Val  
 50 55 60



340 345 350  
 Ser Thr Met Ser Thr Leu Gln Met Ser Leu Gln Ala Glu Ser Lys Ala  
 355 360 365  
 Thr Ile Thr Pro Ser Gly Ser Val Ile Ser Lys Phe Asn Ser Thr Thr  
 370 375 380  
 Ser Ser Ala Thr Pro Gln Ala Phe Asp Ser Ser Ser Ala Val Val Phe  
 385 390 395 400  
 Ile Phe Val Ser Thr Ala Val Val Val Leu Val Ile Leu Thr Met Thr  
 405 410 415  
 Val Leu Gly Leu Val Lys Leu Cys Phe His Glu Ser Pro Ser Ser Gln  
 420 425 430  
 Pro Arg Lys Glu Ser Met Gly Pro Pro Gly Leu Glu Ser Asp Pro Glu  
 435 440 445  
 Pro Ala Ala Leu Gly Ser Ser Ser Ala His Cys Thr Asn Asn Gly Val  
 450 455 460  
 Lys Val Gly Asp Cys Asp Leu Arg Asp Arg Ala Glu Gly Ala Leu Leu  
 465 470 475 480  
 Ala Glu Ser Pro Leu Gly Ser Ser Asp Ala  
 485 490

<210> 97

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 97

tggaaggaga tgcgatgcca cctg

24

<210> 98

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 98

tgaccagtgg ggaaggacag

20





&lt;400&gt; 103

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cggacgcgtg ggattcagca gtggcctgtg gctgccagag cagctcctca ggggaaacta 60
agcgctcgagt cagacggcac cataatcgcc tttaaaagtg cctccgccct gccggccgcg 120
tatccccggg ctacctgggc cgccccgcgg cggtgcgcg cgtgagagggg gcgcgcgggc 180
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cagctctcgc ggcagcagtc cccagagaga cctgttttca catgtggtgg cattcttact 420
ggagagtctg gatttatttg cagtgaaggt tttcctggag tgtaccctcc aaatagcaaa 480
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tctaaatcaa tgcttaataa aatattttta aaggaaaaaa aaaaaa 2026

```

&lt;210&gt; 104

&lt;211&gt; 415

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 104

```

Met Arg Gly Ala Asn Ala Trp Ala Pro Leu Cys Leu Leu Leu Ala Ala
  1              5              10              15

```

```

Ala Thr Gln Leu Ser Arg Gln Gln Ser Pro Glu Arg Pro Val Phe Thr
      20              25              30

```

```

Cys Gly Gly Ile Leu Thr Gly Glu Ser Gly Phe Ile Gly Ser Glu Gly
      35              40              45

```

```

Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr Trp Lys Ile Thr
      50              55              60

```

Val Pro Glu Gly Lys Val Val Val Leu Asn Phe Arg Phe Ile Asp Leu  
 65 70 75 80  
 Glu Ser Asp Asn Leu Cys Arg Tyr Asp Phe Val Asp Val Tyr Asn Gly  
 85 90 95  
 His Ala Asn Gly Gln Arg Ile Gly Arg Phe Cys Gly Thr Phe Arg Pro  
 100 105 110  
 Gly Ala Leu Val Ser Ser Gly Asn Lys Met Met Val Gln Met Ile Ser  
 115 120 125  
 Asp Ala Asn Thr Ala Gly Asn Gly Phe Met Ala Met Phe Ser Ala Ala  
 130 135 140  
 Glu Pro Asn Glu Arg Gly Asp Gln Tyr Cys Gly Gly Leu Leu Asp Arg  
 145 150 155 160  
 Pro Ser Gly Ser Phe Lys Thr Pro Asn Trp Pro Asp Arg Asp Tyr Pro  
 165 170 175  
 Ala Gly Val Thr Cys Val Trp His Ile Val Ala Pro Lys Asn Gln Leu  
 180 185 190  
 Ile Glu Leu Lys Phe Glu Lys Phe Asp Val Glu Arg Asp Asn Tyr Cys  
 195 200 205  
 Arg Tyr Asp Tyr Val Ala Val Phe Asn Gly Gly Glu Val Asn Asp Ala  
 210 215 220  
 Arg Arg Ile Gly Lys Tyr Cys Gly Asp Ser Pro Pro Ala Pro Ile Val  
 225 230 235 240  
 Ser Glu Arg Asn Glu Leu Leu Ile Gln Phe Leu Ser Asp Leu Ser Leu  
 245 250 255  
 Thr Ala Asp Gly Phe Ile Gly His Tyr Ile Phe Arg Pro Lys Lys Leu  
 260 265 270  
 Pro Thr Thr Thr Glu Gln Pro Val Thr Thr Thr Phe Pro Val Thr Thr  
 275 280 285  
 Gly Leu Lys Pro Thr Val Ala Leu Cys Gln Gln Lys Cys Arg Arg Thr  
 290 295 300  
 Gly Thr Leu Glu Gly Asn Tyr Cys Ser Ser Asp Phe Val Leu Ala Gly  
 305 310 315 320  
 Thr Val Ile Thr Thr Ile Thr Arg Asp Gly Ser Leu His Ala Thr Val  
 325 330 335  
 Ser Ile Ile Asn Ile Tyr Lys Glu Gly Asn Leu Ala Ile Gln Gln Ala

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 340 |     | 345 |     | 350 |     |     |     |     |     |     |     |     |     |     |
| Gly | Lys | Asn | Met | Ser | Ala | Arg | Leu | Thr | Val | Val | Cys | Lys | Gln | Cys | Pro |
|     | 355 |     |     |     |     |     | 360 |     |     |     | 365 |     |     |     |     |
| Leu | Leu | Arg | Arg | Gly | Leu | Asn | Tyr | Ile | Ile | Met | Gly | Gln | Val | Gly | Glu |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Asp | Gly | Arg | Gly | Lys | Ile | Met | Pro | Asn | Ser | Phe | Ile | Met | Met | Phe | Lys |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Thr | Lys | Asn | Gln | Lys | Leu | Leu | Asp | Ala | Leu | Lys | Asn | Lys | Gln | Cys |     |
|     |     |     | 405 |     |     |     |     |     | 410 |     |     |     |     | 415 |     |

&lt;210&gt; 105

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 105

ccgattcata gacctcgaga gt

22

&lt;210&gt; 106

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 106

gtcaaggagt cctccacaat ac

22

&lt;210&gt; 107

&lt;211&gt; 45

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 107

gtgtacaatg gccatgccaa tggccagcgc attggccgct tctgt

45

&lt;210&gt; 108

&lt;211&gt; 1838

&lt;212&gt; DNA

T03T20"9905050

<213> Homo sapiens

<400> 108

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cggacgcgtg ggcggacgcg tgggcggccc acggcggccc cgggctgggg cggtcgcttc 60
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aagggcctag tcccagctgt gctctggggc ctacagcctct tcctcaacct cccaggacct 180
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gccccggacc tcttccagtg gctgtgtctc gattccctga agctctgctg ccccgaggc 540
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<210> 109

<211> 420

<212> PRT

<213> Homo sapiens

<400> 109

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Met Ala Pro Trp Pro Pro Lys Gly Leu Val Pro Ala Val Leu Trp Gly
  1                      5                      10                     15

Leu Ser Leu Phe Leu Asn Leu Pro Gly Pro Ile Trp Leu Gln Pro Ser
      20                      25                     30

Pro Pro Pro Gln Ser Ser Pro Pro Pro Gln Pro His Pro Cys His Thr
      35                      40                     45

Cys Arg Gly Leu Val Asp Ser Phe Asn Lys Gly Leu Glu Arg Thr Ile
      50                      55                     60

```

Arg Asp Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Glu Asn Leu  
 65 70 75 80  
 Ser Lys Tyr Lys Asp Ser Glu Thr Arg Leu Val Glu Val Leu Glu Gly  
 85 90 95  
 Val Cys Ser Lys Ser Asp Phe Glu Cys His Arg Leu Leu Glu Leu Ser  
 100 105 110  
 Glu Glu Leu Val Glu Ser Trp Trp Phe His Lys Gln Gln Glu Ala Pro  
 115 120 125  
 Asp Leu Phe Gln Trp Leu Cys Ser Asp Ser Leu Lys Leu Cys Cys Pro  
 130 135 140  
 Ala Gly Thr Phe Gly Pro Ser Cys Leu Pro Cys Pro Gly Gly Thr Glu  
 145 150 155 160  
 Arg Pro Cys Gly Gly Tyr Gly Gln Cys Glu Gly Glu Gly Thr Arg Gly  
 165 170 175  
 Gly Ser Gly His Cys Asp Cys Gln Ala Gly Tyr Gly Gly Glu Ala Cys  
 180 185 190  
 Gly Gln Cys Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ala Ser His  
 195 200 205  
 Leu Val Cys Ser Ala Cys Phe Gly Pro Cys Ala Arg Cys Ser Gly Pro  
 210 215 220  
 Glu Glu Ser Asn Cys Leu Gln Cys Lys Lys Gly Trp Ala Leu His His  
 225 230 235 240  
 Leu Lys Cys Val Asp Ile Asp Glu Cys Gly Thr Glu Gly Ala Asn Cys  
 245 250 255  
 Gly Ala Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu Cys Arg  
 260 265 270  
 Asp Cys Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly Pro Gly Arg  
 275 280 285  
 Cys Lys Lys Cys Ser Pro Gly Tyr Gln Gln Val Gly Ser Lys Cys Leu  
 290 295 300  
 Asp Val Asp Glu Cys Glu Thr Glu Val Cys Pro Gly Glu Asn Lys Gln  
 305 310 315 320  
 Cys Glu Asn Thr Glu Gly Gly Tyr Arg Cys Ile Cys Ala Glu Gly Tyr  
 325 330 335  
 Lys Gln Met Glu Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala  
 340 345 350

T00440-9505050

Gly Phe Phe Ser Glu Met Thr Glu Asp Glu Leu Val Val Leu Gln Gln  
 355 360 365

Met Phe Phe Gly Ile Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys  
 370 375 380

Gly Asp Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met  
 385 390 395 400

Thr Gly Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe  
 405 410 415

Ile Lys Gly Arg  
 420

<210> 110

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 110

cctggctatc agcaggtggg ctccaagtgt ctcgatgtgg atgagtgtga

50

<210> 111

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 111

attctgcgtg aacactgagg gc

22

<210> 112

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 112

atctgcttgt agccctcggc ac

22

<210> 113

<211> 1616  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (1461)  
 <223> a, t, c or g

<400> 113  
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<210> 114  
 <211> 366  
 <212> PRT  
 <213> Homo sapiens

<400> 114  
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 1 5 10 15  
 Ser Pro Gly Ala Ala Leu Thr Gly Glu Gln Leu Leu Gly Ser Leu Leu  
 20 25 30  
 Arg Gln Leu Gln Leu Lys Glu Val Pro Thr Leu Asp Arg Ala Asp Met  
 35 40 45





Arg Pro Gln Val Val Ser Leu Pro Asn Met Arg Val Gln Lys Cys Ser  
                   340                  345                  350

Cys Ala Ser Asp Gly Ala Leu Val Pro Arg Arg Leu Gln Pro  
                   355                  360                  365

<210> 115

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
                   oligonucleotide probe

<400> 115

aggactgccca taacttgccct g

21

<210> 116

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
                   oligonucleotide probe

<400> 116

ataggagttg aagcagcgct gc

22

<210> 117

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
                   oligonucleotide probe

<400> 117

tgtgtggaca tagacgagtg ccgctaccgc tactgccagc accgc

45

<210> 118

<211> 1857

<212> DNA

<213> Homo sapiens

<400> 118

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 aaggcgcaag tcgagaggaa actgttgtgc ctctcatat tggcgatcct gttgtgctcc 120  
 ctggcattgg gcagtgttac agtgcactct tctgaacctg aagtcagaat tcttgagaat 180

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aatcctgtga agttgtcctg tgcctactcg ggcttttctt ctccccgtgt ggagtggaaag 240
tttgaccaag gagacaccac cagactcggt tgctataata acaagatcac agtttcctat 300
gaggaccggg tgaccttctt gccaaactgg atcaccttca agtccgtgac acgggaagac 360
actgggacat acacttgtat ggtctctgag gaaggcggca acagctatgg ggaggtcaag 420
gtcaagctca tcgtgcttgt gcctccatcc aagcctacag ttaacatccc ctctctgcc 480
accattggga accgggcagt gctgacatgc tcagaacaag atggttcccc accttctgaa 540
tacacctggg tcaaagatgg gatagtgat cctacgaatc ccaaaagcac cctgccttc 600
agcaactctt cctatgtcct gaatcccaca acaggagagc tggctcttga tcccctgtca 660
gcctctgata ctggagaata cagctgtgag gcacggaatg ggtatgggac acccatgact 720
tcaaagtctg tgcgcattga agctgtggag cggaatgtgg gggcatcgtg ggcagccgtc 780
cttgtaaccc tgattctcct ggggaatctt gtttttggca tctggtttgc ctatagccga 840
ggccactttg acagaacaaa gaaagggact tcgagtaaga aggtgattta cagccagcct 900
agtgcccgaa gtgaaggaga attcaaacag acctcgtcat tcctgggtgt agcctgggtc 960
gctcaccgcc tatcatctgc atttgcctta ctcagggtgt accggactct ggccctgat 1020
gtctgtagtt tcacaggatg ccttatttgt cttctacacc ccacagggcc cctacttct 1080
tcggatgtgt ttttaataat gtcagctatg tgccccatcc tccttcatgc cctccctccc 1140
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tctagagcgg gaattagagg ctagagcggc tgaaatgggt gtttggtgat gacactgggg 1440
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ggagaaaccc tactggaaat acaaagttag ccaggcatgg tgggtgcatgc ctgtagtccc 1800
agctgctcag gagcctggca acaagagcaa aactccagct caaaaaaaaa aaaaaaa 1857

```

<210> 119

<211> 299

<212> PRT

<213> Homo sapiens

<400> 119

```

Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile
  1                      5                      10                      15

```

```

Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His
          20                      25                      30

```

```

Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu
          35                      40                      45

```

```

Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe
          50                      55                      60

```

```

Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr
          65                      70                      75                      80

```

```

Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe
          85                      90                      95

```





## oligonucleotide probe

<400> 125  
actcagcagt ggtaggaaag

20

<210> 126  
<211> 1210  
<212> DNA  
<213> Homo sapiens

<400> 126  
cagcgcgtgg ccggcgccgc tgtggggaca gcatgagcgg cggttggatg gcgcaggttg 60  
gagcgtggcg aacaggggct ctgggcctgg cgctgctgct gctgctcggc ctcggaactag 120  
gcctggaggc cgccgcgagc ccgctttcca ccccgacctc tgcccaggcc gcaggcccca 180  
gctcaggctc gtgcccaccc accaagttcc agtgccgcac cagtggctta tgcgtgcccc 240  
tcacctggcg ctgcgacagg gacttggact gcagcgatgg cagcgatgag gaggagtga 300  
ggattgagcc atgtacccag aaagggcaat gcccaccgcc ccctggcctc ccctgcccct 360  
gcaccggcgt cagtgactgc tctgggggaa ctgacaagaa actgcgcaac tgcagccgcc 420  
tggcctgcct agcaggcgag ctccgttgca cgctgagcga tgactgcatt ccactcacgt 480  
ggcgtgcga cggccaccca gactgtcccg actccagcga cgagctcggc tgtggaacca 540  
atgagatcct cccggaaggg gatgccacaa ccatggggcc ccctgtgacc ctggagagt 600  
tcacctctct caggaatgcc acaaccatgg ggccccctgt gaccctggag agtgtcccct 660  
ctgtcgggaa tgccacatcc tcctctgccg gagaccagtc tgggaagcca actgcctatg 720  
gggttattgc agctgctgcg gtgctcagtg caagcctggt caccgccacc ctctctcttt 780  
tgtcctggct ccgagcccag gaggcctcc gcccaactggg gttactggtg gccatgaagg 840  
agtccctgct gctgtcagaa cagaagacct cgctgccctg aggacaagca cttgccacca 900  
ccgtcactca gccctgggag tagccggaca ggaggagagc agtgatgcgg atgggtaccc 960  
gggcacacca gccctcagag acctgagttc ttctggccac gtggaacctc gaaccgcagc 1020  
tcctgcagaa gtggccctgg agattgaggg tccttgagca ctccctatgg agatccgggg 1080  
agctaggatg gggaaacctgc cacagccaga actgagggggc tggccccagg cagctcccag 1140  
ggggtagaac ggccctgtgc ttaagacact ccctgctgcc ccgtctgagg gtggcgatta 1200  
aagttgcttc 1210

<210> 127  
<211> 282  
<212> PRT  
<213> Homo sapiens

<400> 127  
Met Ser Gly Gly Trp Met Ala Gln Val Gly Ala Trp Arg Thr Gly Ala  
1 5 10 15  
Leu Gly Leu Ala Leu Leu Leu Leu Gly Leu Gly Leu Gly Leu Glu  
20 25 30  
Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly  
35 40 45  
Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser  
50 55 60  
Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys  
65 70 75 80

090506-0404  
T02740-9305060

<210> 129

<211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 129  
 ttggttccac agccgagctc gtcg 24

<210> 130  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 130  
 gaggaggagt gcaggattga gccatgtacc cagaaagggc aatgcccacc 50

<210> 131  
 <211> 1843  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (1837)  
 <223> a, t, c or g

<400> 131  
 cccacgcgtc cggctctcgct cgctcgcgca gcggcggcag cagaggtcgc gcacagatgc 60  
 gggtagact ggcgggggga ggaggcggag gaggggaagga agctgcatgc atgagaccca 120  
 cagactcttg caagctggat gccctctgtg gatgaaagat gtatcatgga atgaaccaga 180  
 gcaatggaga tggatttcta gagcagcagc agcagcagca gcaacctcag tccccccaga 240  
 gactcttggc cgtgatcctg tggtttcagc tggcgcgtgtg cttcggccct gcacagctca 300  
 cgggcggggt cgtgacactt caagtgtgtg ctgaccccg cttcccgag aatggcttca 360  
 ggacccccag cggagggggt ttctttgaag gctctgtagc ccgatttcac tgccaagacg 420  
 gattcaagct gaagggcgct acaaagagac tgtgtttgaa gcattttaat ggaaccctag 480  
 gctggatccc aagtataat tccatctgtg tgcaagaaga ttgccgtatc cctcaaatac 540  
 aagatgctga gattcataac aagacatata gacatggaga gaagctaata atcacttgct 600  
 atgaaggatt caagatccgg taccgccacc tacacaatat ggtttcatta tgcgcgatg 660  
 atggaacgtg gaataatctg cccatctgtc aaggctgcct gagacctcta gcctcttcta 720  
 atggctatgt aaacatctct gagctccaga cctccttccc ggtggggact gtgatctcct 780  
 atcgtgctt tcccggattt aaacttgatg ggtctgcgta tcttgagtgc ttacaaaacc 840  
 ttatctggtc gtccagccca ccccggtgcc ttgctctgga agcccaagtc tgtccactac 900  
 ctccaatggt gaggcacgga gatttcgtct gccaccgcg gccttgtagc cgctacaacc 960  
 acggaactgt ggtggagttt tactgcgac ctggctacag cctcaccagc gactacaagt 1020  
 acatcacctg ccagtatgga gagggtttc cttcttatca agtctactgc atcaaatcag 1080  
 agcaaacgtg gccagcacc catgagaccc tctgaccac gtggaagatt gtggcggttca 1140



```

cggaaccag tgtgctgctg gtgctgctgc tcgtcatcct ggccaggatg ttccagacca 1200
agttcaaggc ccactttccc cccagggggc ctccccggag ttccagcagt gaccctgact 1260
ttgtggtggt agacggcgtg cccgtcatgc tcccgtccta tgacgaagct gtgagtggcg 1320
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tggacgacca gagcccccca gcataccccg gctcagggga cacggacaca ggcccagggg 1440
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ctcccagggtg ccaagagagc acccaccctg cttcggacaa ccctgacata attgccagca 1560
cggcagagga ggtggcatcc accagcccag gcattccatca tgcccactgg gtgttggtcc 1620
taagaaactg attgattaaa aaatttccca aagtgtcctg aagtgtctct tcaaatacat 1680
gttgatctgt ggagttgatt cctttccttc tcttggtttt agacaaatgt aaacaaagct 1740
ctgaccttta aaattgctat gctgatagag tggtaggggc tggaagcttg atcaagtcct 1800
gtttcttctt gacacagact gattaaaaat taaaagnaaa aaa 1843

```

<210> 132

<211> 490

<212> PRT

<213> Homo sapiens

<400> 132

```

Met Tyr His Gly Met Asn Pro Ser Asn Gly Asp Gly Phe Leu Glu Gln
  1              5              10              15

Gln Gln Gln Gln Gln Gln Pro Gln Ser Pro Gln Arg Leu Leu Ala Val
          20              25              30

Ile Leu Trp Phe Gln Leu Ala Leu Cys Phe Gly Pro Ala Gln Leu Thr
          35              40              45

Gly Gly Phe Asp Asp Leu Gln Val Cys Ala Asp Pro Gly Ile Pro Glu
          50              55              60

Asn Gly Phe Arg Thr Pro Ser Gly Gly Val Phe Phe Glu Gly Ser Val
          65              70              75              80

Ala Arg Phe His Cys Gln Asp Gly Phe Lys Leu Lys Gly Ala Thr Lys
          85              90              95

Arg Leu Cys Leu Lys His Phe Asn Gly Thr Leu Gly Trp Ile Pro Ser
          100              105              110

Asp Asn Ser Ile Cys Val Gln Glu Asp Cys Arg Ile Pro Gln Ile Glu
          115              120              125

Asp Ala Glu Ile His Asn Lys Thr Tyr Arg His Gly Glu Lys Leu Ile
          130              135              140

Ile Thr Cys His Glu Gly Phe Lys Ile Arg Tyr Pro Asp Leu His Asn
          145              150              155              160

Met Val Ser Leu Cys Arg Asp Asp Gly Thr Trp Asn Asn Leu Pro Ile
          165              170              175

Cys Gln Gly Cys Leu Arg Pro Leu Ala Ser Ser Asn Gly Tyr Val Asn

```



Ile Ala Ser Thr Ala Glu Glu Val Ala Ser Thr Ser Pro Gly Ile His  
 465 470 475 480

His Ala His Trp Val Leu Phe Leu Arg Asn  
 485 490

<210> 133

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 133

atctcctatc gctgctttcc cgg

23

<210> 134

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 134

agccaggatc gcagtaaaac tcc

23

<210> 135

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 135

atttaaactt gatgggtctg cgtatcttga gtgcttacaa aaccttatct

50

<210> 136

<211> 1815

<212> DNA

<213> Homo sapiens

<400> 136

cccacgcgtc cgctccgcgc cctccccccc gcctcccgtg cggcccgctg gtggcctaga 60  
 gatgctgctg ccgcggttgc agttgtcgcg cagcctctg cccgccagcc cgctccaccg 120  
 ccgtagcgcc cgagtgtcgc ggggcgcacc cgagtcgggc catgaggccg ggaaccgcgc 180  
 tacaggccgt gctgctggcc gtgctgctgg tggggctgcg ggccgcgacg ggtcgcctgc 240  
 tgagtgcctc ggatttggac ctacagaggag ggcagccagt ctgccgggga gggacacaga 300

ggcttgttta taaagtcatt tacttccatg atacttctcg aagactgaac tttgaggaag 360  
 ccaaagaagc ctgcaggagg gatggaggcc agctagtcag catcgagtct gaagatgaac 420  
 agaaactgat agaaaagtcc attgaaaacc tcttgccatc tgatggtgac ttctggattg 480  
 ggctcaggag gcgtgaggag aaacaaagca atagcacagc ctgccaggac ctttatgctt 540  
 ggactgatgg cagcatatca caatttagga actggtatgt ggatgagccg tcctgcggca 600  
 gcgaggtctg cgtgggtcatg taccatcagc catcggcacc cgctggcatc ggaggcccct 660  
 acatgttcca gtggaatgat gaccgggtgca acatgaagaa caatttcatt tgcaaatatt 720  
 ctgatgagaa accagcagtt ccttctagag aagctgaagg tgaggaaaca gagctgacaa 780  
 cacctgtact tccagaagaa acacaggaag aagatgccaa aaaaacattt aaagaaaagta 840  
 gagaagctgc cttgaatctg gctacatcc taatccccag cattcccctt ctctcctcc 900  
 ttgtgggtcac cacagttgta tgttgggtt ggatctgtag aaaaagaaaa cgggagcagc 960  
 cagaccctag cacaagaag caacacacca tctggccctc tcctcaccag ggaaacagcc 1020  
 cggacctaga ggtctacaat gtcataagaa aacaaagcga agctgactta gctgagacc 1080  
 ggccagacct gaagaatatt tcattccgag tgtgttcggg agaagccact cccgatgaca 1140  
 tgtcttgtga ctatgacaac atggctgtga acccatcaga aagtgggtt gtgactctgg 1200  
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 ggaggagtaa ggagtctgga tgggtggaat atgaaatata tggttattag gacataataa 1320  
 aaactgaaac tgacaacaat ggaaaagaaa tgataagcaa aatcctctta ttttctataa 1380  
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 tccccacgac ctctgttgg acccccacgt tttggctgta tcctttatcc cagccagtca 1500  
 tccagctcga ccttatgaga aggtaccttg ccaggtctg gcacatagta gagtctcaat 1560  
 aaatgtcact tgggttggtg tatctaactt ttaagggaca gagctttacc tggcagtgat 1620  
 aaagatgggc tgtggagctt ggaaaaccac ctctgttttc cttgctctat acagcagcac 1680  
 atattatcat acagacagaa aatccagaat cttttcaaag cccacatatg gtagcacagg 1740  
 ttggcctgtg catcggcaat tctcatatct gtttttttca aagaataaaa tcaaataaag 1800  
 agcaggaaaa aaaaa 1815

<210> 137

<211> 382

<212> PRT

<213> Homo sapiens

<400> 137

Met Arg Pro Gly Thr Ala Leu Gln Ala Val Leu Leu Ala Val Leu Leu  
 1 5 10 15

Val Gly Leu Arg Ala Ala Thr Gly Arg Leu Leu Ser Ala Ser Asp Leu  
 20 25 30

Asp Leu Arg Gly Gly Gln Pro Val Cys Arg Gly Gly Thr Gln Arg Pro  
 35 40 45

Cys Tyr Lys Val Ile Tyr Phe His Asp Thr Ser Arg Arg Leu Asn Phe  
 50 55 60

Glu Glu Ala Lys Glu Ala Cys Arg Arg Asp Gly Gly Gln Leu Val Ser  
 65 70 75 80

Ile Glu Ser Glu Asp Glu Gln Lys Leu Ile Glu Lys Phe Ile Glu Asn  
 85 90 95

Leu Leu Pro Ser Asp Gly Asp Phe Trp Ile Gly Leu Arg Arg Arg Glu  
 100 105 110

0905056.071201



<211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 138  
 gttcattgaa aacctcttgc catctgatgg tgacttctgg attgggctca 50

<210> 139  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 139  
 aagccaaaga agcctgcagg aggg 24

<210> 140  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 140  
 cagtccaagc ataaagggtcc tggc 24

<210> 141  
 <211> 1514  
 <212> DNA  
 <213> Homo sapiens

<400> 141  
 ggggtctccc tcagggccgg gaggcacagc ggtccctgct tgctgaaggg ctggatgtac 60  
 gcatccgcag gttcccgcgg acttgggggc gcccgtgag ccccggcgcc cgcagaagac 120  
 ttgtgtttgc ctctgcagc ctcaaccgg agggcagcga gggcctacca ccatgatcac 180  
 ttgtgtgttc agcatgcgct tgtggacccc agtgggcgtc ctgacctcgc tggcgtactg 240  
 cctgcaccag cggcgggtgg ccctggccga gctgcaggag gccgatggcc agtgtccggt 300  
 cgaccgcagc ctgctgaagt tgaaaatggt gcaggctcgtg ttctgacacg gggctcggag 360  
 tcctctcaag ccgctccgcg tggaggagca ggtagagtgg aacccccagc tattagaggt 420  
 cccaccccaa actcagtttg attacacagt caccaatcta gctggtggtc cgaaaccata 480  
 ttctccttac gactctcaat accatgagac caccctgaag gggggcatgt ttgctgggca 540  
 gctgaccaag gtgggcatgc agcaaagtgt tgccttggga gagagactga ggaagaacta 600  
 tgtggaagac attccctttc ttccaccaac cttcaacca caggaggtct ttattcgttc 660  
 cactaacatt tttcggaatc tggagtccac ccgttggttg ctggctgggc ttttccagt 720

```

tcagaaagaa ggacccatca tcatccacac tgatgaagca gattcagaag tcttgtatcc 780
caactaccaa agctgctgga gcctgaggca gagaaccaga ggccggaggc agactgcctc 840
tttacagcca ggaatctcag aggatttgaa aaagggtgaag gacaggatgg gcattgacag 900
tagtgataaa gtggacttct tcatcctcct ggacaacgtg gctgccgagc aggcacacaa 960
cctcccaagc tgcccatgc tgaagagatt tgcacggatg atcgaacaga gagctgtgga 1020
cacatccttg tacatactgc ccaaggaaga cagggaaagt cttcagatgg cagtagggcc 1080
attcctccac atcctagaga gcaacctgct gaaagccatg gactctgcca ctgccccga 1140
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gaccctgggg atttttgacc acaaatggcc accgtttgct gttgacctga ccatggaact 1260
ttaccagcac ctggaatcta aggagtgggt tgtgcagctc tattaccacg ggaaggagca 1320
ggtgccgaga ggttgccctg atgggctctg cccgctggac atgttcttga atgccatgtc 1380
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gcctttatac aatg 1514

```

<210> 142

<211> 428

<212> PRT

<213> Homo sapiens

<400> 142

```

Met Ile Thr Gly Val Phe Ser Met Arg Leu Trp Thr Pro Val Gly Val
  1                      5                      10                      15

```

```

Leu Thr Ser Leu Ala Tyr Cys Leu His Gln Arg Arg Val Ala Leu Ala
          20                      25                      30

```

```

Glu Leu Gln Glu Ala Asp Gly Gln Cys Pro Val Asp Arg Ser Leu Leu
          35                      40                      45

```

```

Lys Leu Lys Met Val Gln Val Val Phe Arg His Gly Ala Arg Ser Pro
          50                      55                      60

```

```

Leu Lys Pro Leu Pro Leu Glu Glu Gln Val Glu Trp Asn Pro Gln Leu
          65                      70                      75                      80

```

```

Leu Glu Val Pro Pro Gln Thr Gln Phe Asp Tyr Thr Val Thr Asn Leu
          85                      90                      95

```

```

Ala Gly Gly Pro Lys Pro Tyr Ser Pro Tyr Asp Ser Gln Tyr His Glu
          100                      105                      110

```

```

Thr Thr Leu Lys Gly Gly Met Phe Ala Gly Gln Leu Thr Lys Val Gly
          115                      120                      125

```

```

Met Gln Gln Met Phe Ala Leu Gly Glu Arg Leu Arg Lys Asn Tyr Val
          130                      135                      140

```

```

Glu Asp Ile Pro Phe Leu Ser Pro Thr Phe Asn Pro Gln Glu Val Phe
          145                      150                      155                      160

```

```

Ile Arg Ser Thr Asn Ile Phe Arg Asn Leu Glu Ser Thr Arg Cys Leu
          165                      170                      175

```

Leu Ala Gly Leu Phe Gln Cys Gln Lys Glu Gly Pro Ile Ile Ile His  
                   180                  185                  190  
 Thr Asp Glu Ala Asp Ser Glu Val Leu Tyr Pro Asn Tyr Gln Ser Cys  
                   195                  200                  205  
 Trp Ser Leu Arg Gln Arg Thr Arg Gly Arg Arg Gln Thr Ala Ser Leu  
                   210                  215                  220  
 Gln Pro Gly Ile Ser Glu Asp Leu Lys Lys Val Lys Asp Arg Met Gly  
 225                  230                  235                  240  
 Ile Asp Ser Ser Asp Lys Val Asp Phe Phe Ile Leu Leu Asp Asn Val  
                   245                  250                  255  
 Ala Ala Glu Gln Ala His Asn Leu Pro Ser Cys Pro Met Leu Lys Arg  
                   260                  265                  270  
 Phe Ala Arg Met Ile Glu Gln Arg Ala Val Asp Thr Ser Leu Tyr Ile  
                   275                  280                  285  
 Leu Pro Lys Glu Asp Arg Glu Ser Leu Gln Met Ala Val Gly Pro Phe  
                   290                  295                  300  
 Leu His Ile Leu Glu Ser Asn Leu Leu Lys Ala Met Asp Ser Ala Thr  
 305                  310                  315                  320  
 Ala Pro Asp Lys Ile Arg Lys Leu Tyr Leu Tyr Ala Ala His Asp Val  
                   325                  330                  335  
 Thr Phe Ile Pro Leu Leu Met Thr Leu Gly Ile Phe Asp His Lys Trp  
                   340                  345                  350  
 Pro Pro Phe Ala Val Asp Leu Thr Met Glu Leu Tyr Gln His Leu Glu  
                   355                  360                  365  
 Ser Lys Glu Trp Phe Val Gln Leu Tyr Tyr His Gly Lys Glu Gln Val  
                   370                  375                  380  
 Pro Arg Gly Cys Pro Asp Gly Leu Cys Pro Leu Asp Met Phe Leu Asn  
 385                  390                  395                  400  
 Ala Met Ser Val Tyr Thr Leu Ser Pro Glu Lys Tyr His Ala Leu Cys  
                   405                  410                  415  
 Ser Gln Thr Gln Val Met Glu Val Gly Asn Glu Glu  
                   420                  425

&lt;210&gt; 143

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

09505056.07.201  
 102720" 95050560



<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 143

ccaactacca aagctgctgg agcc

24

<210> 144

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 144

gcagctctat taccacggga agga

24

<210> 145

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 145

tccttcccgt ggtaatagag ctgc

24

<210> 146

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 146

ggcagagaac cagaggccgg aggagactgc ctctttacag ccagg

45

<210> 147

<211> 1686

<212> DNA

<213> Homo sapiens

<400> 147

ctcctcttaa catacttgca gctaaaacta aatattgctg cttggggacc tccttctagc 60  
cttaaatttc agctcatcac cttcacctgc cttgggtcatg gctctgctat ttccttgat 120  
ccttgccatt tgcaccagac ctggattcct agcgtctcca tctggagtgc ggctggtggg 180

09905006-0704

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gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt ggggcaccgt 240
gtgtgatgac ggctgggaca ttaaggacgt ggctgtgttg tgccgggagc tgggctgtgg 300
agctgccagc ggaaccccta gtggtathtt gtatgagcca ccagcagaaa aagagcaaaa 360
ggctctcatc caatcagtca gttgcacagg aacagaagat acattggctc agtgtgagca 420
agaagaagtt tatgattggt cacatgatga agatgctggg gcatcgtgtg agaaccaga 480
gagctctttc tccccagtcc cagaggggtg caggctggct gacggccctg ggcattgcaa 540
gggacgcgtg gaagtgaagc accagaacca gtggtatacc gtgtgccaga caggctggag 600
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tgthtctctg aagaactctg acaaaatata gattttggta ctgaaagaga ttctagagga 1560
acggaattht aaggataaat tttctgaatt ggthtgggg tttctgaaat tggctctata 1620
atctaattag atataaaatt ctgtaactt tatttacaat aataaagata gcactatgtg 1680
ttcaaa 1686

```

<210> 148

<211> 347

<212> PRT

<213> Homo sapiens

<400> 148

Met Ala Leu Leu Phe Ser Leu Ile Leu Ala Ile Cys Thr Arg Pro Gly  
1 5 10 15

Phe Leu Ala Ser Pro Ser Gly Val Arg Leu Val Gly Gly Leu His Arg  
20 25 30

Cys Glu Gly Arg Val Glu Val Glu Gln Lys Gly Gln Trp Gly Thr Val  
35 40 45

Cys Asp Asp Gly Trp Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu  
50 55 60

Leu Gly Cys Gly Ala Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu  
65 70 75 80

Pro Pro Ala Glu Lys Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys  
85 90 95

Thr Gly Thr Glu Asp Thr Leu Ala Gln Cys Glu Gln Glu Glu Val Tyr  
100 105 110

Asp Cys Ser His Asp Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu  
 115 120 125  
 Ser Ser Phe Ser Pro Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro  
 130 135 140  
 Gly His Cys Lys Gly Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr  
 145 150 155 160  
 Thr Val Cys Gln Thr Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys  
 165 170 175  
 Arg Gln Leu Gly Cys Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn  
 180 185 190  
 Lys His Ala Tyr Gly Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys  
 195 200 205  
 Ser Gly Arg Glu Ala Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly  
 210 215 220  
 Lys Asn Thr Cys Asn His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp  
 225 230 235 240  
 Pro Phe Asp Leu Arg Leu Val Gly Gly Asp Asn Leu Cys Ser Gly Arg  
 245 250 255  
 Leu Glu Val Leu His Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn  
 260 265 270  
 Trp Gly Glu Lys Glu Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly  
 275 280 285  
 Lys Ser Leu Ser Pro Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly  
 290 295 300  
 Val Gly Arg Ile Trp Leu Asp Asn Val Arg Cys Ser Gly Glu Glu Gln  
 305 310 315 320  
 Ser Leu Glu Gln Cys Gln His Arg Phe Trp Gly Phe His Asp Cys Thr  
 325 330 335  
 His Gln Glu Asp Val Ala Val Ile Cys Ser Val  
 340 345

<210> 149

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

0905056-071291

<400> 149  
ttcagctcat caccttcacc tgcc 24

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

```
<210> 152
<211> 1427
<212> DNA
<213> Homo sapiens
```

| <400>       | 152         |             |              |            |            |      |  |
|-------------|-------------|-------------|--------------|------------|------------|------|--|
| actgcactcg  | gttctatcga  | ttgaattccc  | cgggggatacct | ctagagatcc | ctcgacctcg | 60   |  |
| acccacgcgt  | ccgcggacgc  | gtgggcggac  | gcgtgggccc   | gctaccagga | agagtctgcc | 120  |  |
| gaagggtgaag | gccatggact  | tcatacctc   | cacagccatc   | ctgcccctgc | tgttcggctg | 180  |  |
| cctgggcgtc  | ttcggcctct  | tccggtctgt  | gcagtgggtg   | cgcgggaagg | cctacctgcg | 240  |  |
| gaatgctgtg  | gtgggtgatca | caggcgccac  | ctcagggctg   | ggcaaagaat | gtgcaaaagt | 300  |  |
| cttctatgct  | gcgggtgcta  | aactgggtgt  | ctgtggccgg   | aatggtgggg | ccctagaaga | 360  |  |
| gctcatcaga  | gaacttaccg  | cttctcatgc  | caccaagggtg  | cagacacaca | agccttactt | 420  |  |
| ggtgaccttc  | gacctcacag  | actctggggc  | catagttgca   | gcagcagctg | agatcctgca | 480  |  |
| gtgctttggc  | tatgtcgaca  | tacttgtcaa  | caatgctggg   | atcagctacc | gtggtagcat | 540  |  |
| catggacacc  | acagtggatg  | tggaacaagag | ggtcatggag   | acaaactact | ttggcccagt | 600  |  |
| tgctctaacg  | aaagcactcc  | tgccctccat  | gatcaagagg   | aggcaaggcc | acattgtcgc | 660  |  |
| catcagcagc  | atccagggga  | agatgagcat  | tcctttttcga  | tcagcatatg | cagcctccaa | 720  |  |
| gcacgcgaac  | caggctttct  | ttgactgtct  | gcgtgccgag   | atggaacagt | atgaaattga | 780  |  |
| ggtgaccgtc  | atcagccccc  | gctacatcca  | caccacacctc  | tctgtaaatg | ccatcacgcg | 840  |  |
| ggatggatct  | aggtatggag  | ttatggacac  | caccacagcc   | cagggccgaa | gccctgtgga | 900  |  |
| ggtggcccag  | gagtgttctg  | ctgctgtggg  | gaagaagaag   | aaagatgtga | tcctggctga | 960  |  |
| cttactgcct  | tccttggtctg | tttatcttog  | aactctggct   | cctgggctct | tcctcagcct | 1020 |  |
| catggcctcc  | agggccagaa  | aagagcggaa  | atccaagaac   | tcctagtact | ctgaccagcc | 1080 |  |

```

agggccaggg cagagaagca gcactcttag gcttgcttac tctacaaggg acagttgcat 1140
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gtgcagatct gctggcagag gacaatcaaa aacgacaaca agcttcttcc cagggtgagg 1260
ggaaacactt aaggaataaa tatggagctg gggtttaaca ctaaaaacta gaaataaaca 1320
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cttggccgcc atggcccaac ttgtttattg cagcttataa tggttac 1427

```

<210> 153

<211> 310

<212> PRT

<213> Homo sapiens

<400> 153

```

Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys
  1             5             10             15

```

```

Leu Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp Val Arg Gly Lys
      20             25             30

```

```

Ala Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly
      35             40             45

```

```

Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu
      50             55             60

```

```

Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu
      65             70             75             80

```

```

Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu
      85             90             95

```

```

Val Thr Phe Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala Ala
      100            105            110

```

```

Glu Ile Leu Gln Cys Phe Gly Tyr Val Asp Ile Leu Val Asn Asn Ala
      115            120            125

```

```

Gly Ile Ser Tyr Arg Gly Thr Ile Met Asp Thr Thr Val Asp Val Asp
      130            135            140

```

```

Lys Arg Val Met Glu Thr Asn Tyr Phe Gly Pro Val Ala Leu Thr Lys
      145            150            155            160

```

```

Ala Leu Leu Pro Ser Met Ile Lys Arg Arg Gln Gly His Ile Val Ala
      165            170            175

```

```

Ile Ser Ser Ile Gln Gly Lys Met Ser Ile Pro Phe Arg Ser Ala Tyr
      180            185            190

```

```

Ala Ala Ser Lys His Ala Thr Gln Ala Phe Phe Asp Cys Leu Arg Ala
      195            200            205

```

```

Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr

```

0950556.07304

|   |     |         |
|---|-----|---------|
| 210   | 215 | 220     |
| Ile His Thr Asn Leu Ser Val Asn Ala Ile Thr Ala Asp Gly Ser Arg |     |         |
| 225   | 230 | 235 240 |
| Tyr Gly Val Met Asp Thr Thr Thr Ala Gln Gly Arg Ser Pro Val Glu |     |         |
|   | 245 | 250 255 |
| Val Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys Lys Asp Val |     |         |
|   | 260 | 265 270 |
| Ile Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu Arg Thr Leu |     |         |
|   | 275 | 280 285 |
| Ala Pro Gly Leu Phe Phe Ser Leu Met Ala Ser Arg Ala Arg Lys Glu |     |         |
|   | 290 | 300     |

Arg Lys Ser Lys Asn Ser  
305 310

<210> 154

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 154

ggtgctaaac tggtgctctg tggc

24

<210> 155

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 155

cagggcaaga tgagcattcc

20

<210> 156

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 156  
tcatactggt ccactctggc acgc 24

<210> 157

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 157  
aatggtgggg ccctagaaga gctcatcaga gaactcaccg cttctcatgc 50

<210> 158

<211> 1771

<212> DNA

<213> Homo sapiens

<400> 158  
cccacgcgctc cgctgggtgtt agatcgagca accctctaaa agcagtttag agtggtaaaa 60  
aaaaaaaaaa acacacccaaa cgctcgagc caaaaaggg atgaaatttc ttctggacat 120  
cctcctgctt ctcccgttac tgatcgctctg ctccctagag tccttcgtga agctttttat 180  
tcctaagagg agaaaatcag tcaccggcga aatcgctgtg attacaggag ctgggcatgg 240  
aattgggaga ctgactgcct atgaatttgc taaacttaaa agcaagctgg ttctctggga 300  
tataaataag catggactgg aggaaacagc tgccaaatgc aagggactgg gtgccaagg 360  
tcataccttt gtggtagact gcagcaaccg agaagatatt tacagctctg caaagaagg 420  
gaaggcagaa attggagatg ttagtatttt agtaaataat gctgggttag tctatacatc 480  
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aagcaagttt gctgctgttg gatttcataa aactttgaca gatgaactgg ctgccttaca 720  
aataactgga gtcaaaacaa catgtctgtg tcctaatttc gtaaacactg gcttcatcaa 780  
aaatccaagt acaagtttgg gaccactctt ggaacctgag gaagtggtaa acaggctgat 840  
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1740  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 1771

<210> 159

<211> 300  
 <212> PRT  
 <213> Homo sapiens

<400> 159

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Phe | Leu | Leu | Asp | Ile | Leu | Leu | Leu | Leu | Pro | Leu | Leu | Ile | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Cys | Ser | Leu | Glu | Ser | Phe | Val | Lys | Leu | Phe | Ile | Pro | Lys | Arg | Arg | Lys |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Val | Thr | Gly | Glu | Ile | Val | Leu | Ile | Thr | Gly | Ala | Gly | His | Gly | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Arg | Leu | Thr | Ala | Tyr | Glu | Phe | Ala | Lys | Leu | Lys | Ser | Lys | Leu | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Trp | Asp | Ile | Asn | Lys | His | Gly | Leu | Glu | Glu | Thr | Ala | Ala | Lys | Cys |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Lys | Gly | Leu | Gly | Ala | Lys | Val | His | Thr | Phe | Val | Val | Asp | Cys | Ser | Asn |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Arg | Glu | Asp | Ile | Tyr | Ser | Ser | Ala | Lys | Lys | Val | Lys | Ala | Glu | Ile | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asp | Val | Ser | Ile | Leu | Val | Asn | Asn | Ala | Gly | Val | Val | Tyr | Thr | Ser | Asp |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Phe | Ala | Thr | Gln | Asp | Pro | Gln | Ile | Glu | Lys | Thr | Phe | Glu | Val | Asn |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Leu | Ala | His | Phe | Trp | Thr | Thr | Lys | Ala | Phe | Leu | Pro | Ala | Met | Thr |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Lys | Asn | Asn | His | Gly | His | Ile | Val | Thr | Val | Ala | Ser | Ala | Ala | Gly | His |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Val | Ser | Val | Pro | Phe | Leu | Leu | Ala | Tyr | Cys | Ser | Ser | Lys | Phe | Ala | Ala |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Val | Gly | Phe | His | Lys | Thr | Leu | Thr | Asp | Glu | Leu | Ala | Ala | Leu | Gln | Ile |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Thr | Gly | Val | Lys | Thr | Thr | Cys | Leu | Cys | Pro | Asn | Phe | Val | Asn | Thr | Gly |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Phe | Ile | Lys | Asn | Pro | Ser | Thr | Ser | Leu | Gly | Pro | Thr | Leu | Glu | Pro | Glu |
|     | 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Glu | Val | Val | Asn | Arg | Leu | Met | His | Gly | Ile | Leu | Thr | Glu | Gln | Lys | Met |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |

099050506 074204



Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln  
290 295 300

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

23

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

24

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

48

<213> Homo sapiens

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tcagggagqa qcaccgactg cgccgcaccc tgagagatgg ttggtgccat gtggaagggtg 120
```

```

attgttttcg tggtcctgtt gatgcctggc ccctgtgatg ggctgtttcg ctccctatac 180
agaagtgttt ccatgccacc taaggagac tcaggacagc cattatttct cacccttac 240
attgaagctg ggaagatcca aaaaggaaga gaattgagtt tggtcggccc tttcccagga 300
ctgaacatga agagtatatc cggcttcctc accgtgaata agacttaca cagcaacctc 360
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ctttacattg acaatccagt gggcacaggc ttcagtttta ctgatgatac ccacggatat 600
gcagtcaatg aggacgatgt agcacgggat ttatacagtg cactaattca gtttttccag 660
atatttcctg aatataaaaa taatgacttt tatgtcactg gggagtctta tgcagggaaa 720
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tcatatctgc aagatTTTTT tcatcaataa aaattatcct tgaaacaagt gagcttttgt 1680
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```

```

<210> 164
<211> 476
<212> PRT
<213> Homo sapiens

```

```

<400> 164
Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu Leu Met
  1             5             10             15

Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser Val Ser
      20             25             30

Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr
      35             40             45

Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly
      50             55             60

Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val

```

|   |   |    |  |     |  |     |
|---|---|----|--|-----|--|-----|
| 65  |   | 70 |  | 75  |  | 80  |
| Asn Lys Thr Tyr   | Asn Ser Asn Leu Phe Phe Trp Phe Phe Pro Ala Gln |    |  |     |  |     |
|   | 85  |    |  | 90  |  | 95  |
| Ile Gln Pro Glu Asp Ala Pro Val Val Leu Trp Leu Gln Gly Gly Pro |   |    |  |     |  |     |
|   | 100   |    |  | 105 |  | 110 |
| Gly Gly Ser Ser Met Phe Gly Leu Phe Val Glu His Gly Pro Tyr Val |   |    |  |     |  |     |
|   | 115   |    |  | 120 |  | 125 |
| Val Thr Ser Asn Met Thr Leu Arg Asp Arg Asp Phe Pro Trp Thr Thr |   |    |  |     |  |     |
|   | 130   |    |  | 135 |  | 140 |
| Thr Leu Ser Met Leu Tyr Ile Asp Asn Pro Val Gly Thr Gly Phe Ser |   |    |  |     |  |     |
|   | 145   |    |  | 150 |  | 155 |
| Phe Thr Asp Asp Thr His Gly Tyr Ala Val Asn Glu Asp Asp Val Ala |   |    |  |     |  |     |
|   |   |    |  | 165 |  | 170 |
| Arg Asp Leu Tyr Ser Ala Leu Ile Gln Phe Phe Gln Ile Phe Pro Glu |   |    |  |     |  |     |
|   |   |    |  | 180 |  | 185 |
| Tyr Lys Asn Asn Asp Phe Tyr Val Thr Gly Glu Ser Tyr Ala Gly Lys |   |    |  |     |  |     |
|   |   |    |  | 195 |  | 200 |
| Tyr Val Pro Ala Ile Ala His Leu Ile His Ser Leu Asn Pro Val Arg |   |    |  |     |  |     |
|   |   |    |  | 210 |  | 215 |
| Glu Val Lys Ile Asn Leu Asn Gly Ile Ala Ile Gly Asp Gly Tyr Ser |   |    |  |     |  |     |
|   |   |    |  | 225 |  | 230 |
| Asp Pro Glu Ser Ile Ile Gly Gly Tyr Ala Glu Phe Leu Tyr Gln Ile |   |    |  |     |  |     |
|   |   |    |  | 245 |  | 250 |
| Gly Leu Leu Asp Glu Lys Gln Lys Lys Tyr Phe Gln Lys Gln Cys His |   |    |  |     |  |     |
|   |   |    |  | 260 |  | 265 |
| Glu Cys Ile Glu His Ile Arg Lys Gln Asn Trp Phe Glu Ala Phe Glu |   |    |  |     |  |     |
|   |   |    |  | 275 |  | 280 |
| Ile Leu Asp Lys Leu Leu Asp Gly Asp Leu Thr Ser Asp Pro Ser Tyr |   |    |  |     |  |     |
|   |   |    |  | 290 |  | 295 |
| Phe Gln Asn Val Thr Gly Cys Ser Asn Tyr Tyr Asn Phe Leu Arg Cys |   |    |  |     |  |     |
|   |   |    |  | 305 |  | 310 |
| Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val Lys Phe Leu Ser Leu Pro |   |    |  |     |  |     |
|   |   |    |  | 325 |  | 330 |
| Glu Val Arg Gln Ala Ile His Val Gly Asn Gln Thr Phe Asn Asp Gly |   |    |  |     |  |     |
|   |   |    |  | 340 |  | 345 |
|   |   |    |  |     |  | 350 |

09905056-07394



<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 167

agctctcaga ggctggtcat aggg

24

<210> 168

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 168

gtcggccctt tcccaggact gaacatgaag agttatgccg gcttctcac

50

<210> 169

<211> 2477

<212> DNA

<213> Homo sapiens

<400> 169

|             |            |            |             |             |             |      |
|-------------|------------|------------|-------------|-------------|-------------|------|
| cgagggttt   | tccggtccg  | gaatggcaca | tgtgggaatc  | ccagtcttgt  | tggctacaac  | 60   |
| atTTTTccct  | ttcctaacaa | gttctaacag | ctgttctaac  | agctagtgat  | caggggttct  | 120  |
| tcttgctgga  | gaagaaagg  | ctgagggcag | agcagggcac  | tctcactcag  | ggtgaccagc  | 180  |
| tccttgccctc | tctgtggata | acagagcatg | agaaagtga   | gagatgcagc  | ggagtgaggt  | 240  |
| gatggaagtc  | taaaatagga | aggaatTTTg | tgtgcaatat  | cagactctgg  | gagcagttga  | 300  |
| cctggagagc  | ctgggggagg | gcctgcctaa | caagctttca  | aaaaacagga  | gcgacttcca  | 360  |
| ctgggctggg  | ataagacgtg | ccggtaggat | aggggaagact | gggttttagtc | ctaatatcaa  | 420  |
| attgactggc  | tgggtgaact | tcaacagcct | tttaacctct  | ctgggagatg  | aaaacgatgg  | 480  |
| cttaaggggc  | cagaaataga | gatgctttgt | aaaataaaat  | tttaaaaaaa  | gcaagtattt  | 540  |
| tatagcataa  | aggctagaga | ccaaaataga | taacaggatt  | ccctgaacat  | tcctaagagg  | 600  |
| gagaaagtat  | gttaaaaata | gaaaaaccaa | aatgcagaag  | gaggagactc  | acagagctaa  | 660  |
| accaggatgg  | ggaccttggg | tcaggccagc | ctctttgctc  | ctcccgaaa   | ttatttttgg  | 720  |
| tctgaccact  | ctgccttggt | ttttgcagaa | tcattgtgagg | gccaaccggg  | gaaggtggag  | 780  |
| cagatgagca  | cacacaggag | ccgtctcctc | accgccgccc  | ctctcagcat  | ggaacagagg  | 840  |
| cagccctggc  | cccgggccct | ggaggtggac | agccgctctg  | tggtcctgct  | ctcagtggtc  | 900  |
| tgggtgctgc  | tggccccccc | agcagccggc | atgcctcagt  | tcagcacctt  | ccactctgag  | 960  |
| aatcgtgact  | ggaccttcaa | ccacttgacc | gtccaccaag  | ggacgggggc  | cgtctatgtg  | 1020 |
| ggggccatca  | accgggtcta | taagctgaca | ggcaacctga  | ccatccaggt  | ggctcataag  | 1080 |
| acagggccag  | aagaggacaa | caagtctcgt | taccgcgcc   | tcactcgtga  | gccctgcagc  | 1140 |
| gaagtgtca   | ccctcaccaa | caatgtcaac | aagctgtctca | tcattgacta  | ctctgagaac  | 1200 |
| cgctgtctgg  | cctgtgggag | cctctaccag | ggggtctgca  | agctgctgcg  | gctggatgac  | 1260 |
| ctcttcatcc  | tgggtggagc | atcccaaca  | agggagcact  | acctgtccag  | tgtcaacaag  | 1320 |
| acgggcacca  | tgtacggggt | gattgtgccc | tctgaggggtg | aggatggcaa  | gctcttcac   | 1380 |
| ggcacggctg  | tggatgggaa | gcaggattac | ttcccgaccc  | tgtccagccg  | gaagctgccc  | 1440 |
| cgagaccctg  | agtctcagc  | catgctcgac | tatgagctac  | acagcgattt  | tgtctcctct  | 1500 |
| ctcatcaaga  | tccttcaga  | cacctggcc  | ctggctctcc  | actttgacat  | cttctacatc  | 1560 |
| tacggctttg  | ctagtggggg | ctttgtctac | tttctcactg  | tccagccga   | gaccctgag   | 1620 |
| gggtgtggcca | tcaactccgc | tggagacctc | ttctacacct  | cacgcacgt   | gcggtctctgc | 1680 |

```

<210> 170
<211> 552
<212> PRT
<213> Homo sapiens

<400> 170
Met Gly Thr Leu Gly Gln Ala Ser Leu Phe Ala Pro Pro Gly Asn Tyr
 1             5             10             15
Phe Trp Ser Asp His Ser Ala Leu Cys Phe Ala Glu Ser Cys Glu Gly
      20             25             30
Gln Pro Gly Lys Val Glu Gln Met Ser Thr His Arg Ser Arg Leu Leu
      35             40             45
Thr Ala Ala Pro Leu Ser Met Glu Gln Arg Gln Pro Trp Pro Arg Ala
      50             55             60
Leu Glu Val Asp Ser Arg Ser Val Val Leu Leu Ser Val Val Trp Val
      65             70             75             80
Leu Leu Ala Pro Pro Ala Ala Gly Met Pro Gln Phe Ser Thr Phe His
      85             90             95
Ser Glu Asn Arg Asp Trp Thr Phe Asn His Leu Thr Val His Gln Gly
      100            105            110
Thr Gly Ala Val Tyr Val Gly Ala Ile Asn Arg Val Tyr Lys Leu Thr
      115            120            125
Gly Asn Leu Thr Ile Gln Val Ala His Lys Thr Gly Pro Glu Glu Asp
      130            135            140
Asn Lys Ser Arg Tyr Pro Pro Leu Ile Val Gln Pro Cys Ser Glu Val
      145            150            155            160
Leu Thr Leu Thr Asn Asn Val Asn Lys Leu Leu Ile Ile Asp Tyr Ser
      165            170            175

```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Asn | Arg | Leu | Leu | Ala | Cys | Gly | Ser | Leu | Tyr | Gln | Gly | Val | Cys | Lys |     |
|     |     |     | 180 |     |     |     | 185 |     |     | 190 |     |     |     |     |     |     |
| Leu | Leu | Arg | Leu | Asp | Asp | Leu | Phe | Ile | Leu | Val | Glu | Pro | Ser | His | Lys |     |
|     |     |     | 195 |     |     |     | 200 | 205 |     |     |     |     |     |     |     |     |
| Lys | Glu | His | Tyr | Leu | Ser | Ser | Val | Asn | Lys | Thr | Gly | Thr | Met | Tyr | Gly |     |
|     |     |     | 210 | 215 |     |     | 220 |     |     |     |     |     |     |     |     |     |
| Val | Ile | Val | Arg | Ser | Glu | Gly | Glu | Asp | Gly | Lys | Leu | Phe | Ile | Gly | Thr |     |
| 225 |     |     |     | 230 |     |     | 235 |     |     |     |     |     |     |     |     | 240 |
| Ala | Val | Asp | Gly | Lys | Gln | Asp | Tyr | Phe | Pro | Thr | Leu | Ser | Ser | Arg | Lys |     |
|     |     |     | 245 |     |     | 250 |     |     | 255 |     |     |     |     |     |     |     |
| Leu | Pro | Arg | Asp | Pro | Glu | Ser | Ser | Ala | Met | Leu | Asp | Tyr | Glu | Leu | His |     |
|     |     |     | 260 |     |     | 265 |     |     | 270 |     |     |     |     |     |     |     |
| Ser | Asp | Phe | Val | Ser | Ser | Leu | Ile | Lys | Ile | Pro | Ser | Asp | Thr | Leu | Ala |     |
|     |     |     | 275 |     |     | 280 |     |     | 285 |     |     |     |     |     |     |     |
| Leu | Val | Ser | His | Phe | Asp | Ile | Phe | Tyr | Ile | Tyr | Gly | Phe | Ala | Ser | Gly |     |
|     |     |     | 290 |     |     | 295 |     |     | 300 |     |     |     |     |     |     |     |
| Gly | Phe | Val | Tyr | Phe | Leu | Thr | Val | Gln | Pro | Glu | Thr | Pro | Glu | Gly | Val |     |
| 305 |     |     |     | 310 |     |     | 315 |     |     |     |     |     |     |     |     | 320 |
| Ala | Ile | Asn | Ser | Ala | Gly | Asp | Leu | Phe | Tyr | Thr | Ser | Arg | Ile | Val | Arg |     |
|     |     |     | 325 |     |     | 330 |     |     | 335 |     |     |     |     |     |     |     |
| Leu | Cys | Lys | Asp | Asp | Pro | Lys | Phe | His | Ser | Tyr | Val | Ser | Leu | Pro | Phe |     |
|     |     |     | 340 |     |     | 345 |     |     | 350 |     |     |     |     |     |     |     |
| Gly | Cys | Thr | Arg | Ala | Gly | Val | Glu | Tyr | Arg | Leu | Leu | Gln | Ala | Ala | Tyr |     |
|     |     |     | 355 |     |     | 360 |     |     | 365 |     |     |     |     |     |     |     |
| Leu | Ala | Lys | Pro | Gly | Asp | Ser | Leu | Ala | Gln | Ala | Phe | Asn | Ile | Thr | Ser |     |
|     |     |     | 370 |     |     | 375 |     |     | 380 |     |     |     |     |     |     |     |
| Gln | Asp | Asp | Val | Leu | Phe | Ala | Ile | Phe | Ser | Lys | Gly | Gln | Lys | Gln | Tyr |     |
| 385 |     |     |     | 390 |     |     | 395 |     |     |     |     |     |     |     |     | 400 |
| His | His | Pro | Pro | Asp | Asp | Ser | Ala | Leu | Cys | Ala | Phe | Pro | Ile | Arg | Ala |     |
|     |     |     | 405 |     |     | 410 |     |     | 415 |     |     |     |     |     |     |     |
| Ile | Asn | Leu | Gln | Ile | Lys | Glu | Arg | Leu | Gln | Ser | Cys | Tyr | Gln | Gly | Glu |     |
|     |     |     | 420 |     |     | 425 |     |     | 430 |     |     |     |     |     |     |     |
| Gly | Asn | Leu | Glu | Leu | Asn | Trp | Leu | Leu | Gly | Lys | Asp | Val | Gln | Cys | Thr |     |
|     |     |     | 435 |     |     | 440 |     |     | 445 |     |     |     |     |     |     |     |
| Lys | Ala | Pro | Val | Pro | Ile | Asp | Asp | Asn | Phe | Cys | Gly | Leu | Asp | Ile | Asn |     |

450                      455                      460  
 Gln Pro Leu Gly Gly Ser Thr Pro Val Glu Gly Leu Thr Leu Tyr Thr  
 465                      470                      475                      480  
 Thr Ser Arg Asp Arg Met Thr Ser Val Ala Ser Tyr Val Tyr Asn Gly  
                     485                      490                      495  
 Tyr Ser Val Val Phe Val Gly Thr Lys Ser Gly Lys Leu Lys Lys Val  
                     500                      505                      510  
 Arg Val Tyr Glu Phe Arg Cys Ser Asn Ala Ile His Leu Leu Ser Lys  
                     515                      520                      525  
 Glu Ser Leu Leu Glu Gly Ser Tyr Trp Trp Arg Phe Asn Tyr Arg Gln  
                     530                      535                      540  
 Leu Tyr Phe Leu Gly Glu Gln Arg  
 545                      550

<210> 171

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 171

tggaataaccg cctcctgcag

20

<210> 172

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 172

cttctgcctt ttggagaaga tggc

24

<210> 173

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe



<400> 173  
ggactcactg gccagggcct tcaatatcac cagccaggac gat 42

<210> 174  
<211> 3106  
<212> DNA  
<213> Homo sapiens

<220>  
<221> modified\_base  
<222> (1683)  
<223> a, t, c or g

<400> 174  
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aacacgcgat gaccacgtgg agcctccggc ggaggccggc ccgcacgctg ggactcctgc 120  
tgetggctgt cttgggcttc ctgggtctec gcaggctgga ctggagcacc ctggctccctc 180  
tgcggtcccg ccacgcacag ctggggctgc aggccaaggg ctggaacttc atgctggagg 240  
attccacctt ctggatcttc gggggctcca tccactattt ccgtgtgccc agggagtact 300  
ggagggaccg cctgctgaag atgaaggcct gtggcttgaa caccctcacc acctatgttc 360  
cgtggaacct gcatgagcca gaaagaggca aatttgactt ctctgggaac ctggacctgg 420  
aggccttcgt cctgatggcc gcagagatcg ggctgtgggt gattctgctg ccaggccctt 480  
acatctgcag tgagatggac ctggggggct tgcccagctg gctactccaa gaccctggca 540  
tgaggtctgag gacaacttac aagggtctca ccgaagcagt ggacctttat tttgaccacc 600  
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tgagagaatga atatggttcc tataataaag accccgcata catgccctac gtcaagaagg 720  
cactggagga ccgtggcatt gtggaactgc tcctgacttc agacaacaag gatgggctga 780  
gcaaggggat tgtccaggga gtcttgggca ccatcaactt gcagtcaaca cagagctgc 840  
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ggatggctct gggcctggct ttgttgatga tggctttcct acagccctgc tcttgtgccg 2220  
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```

cagaaaaagt gctgaaacgt gcccttgac cggacgtcac agccctgcga gcctctgctg 2340
gactcaggcg tgctctttgc tggttcctgg gaggttggc cacatccctc atggcccat 2400
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gaagtgtgtc caagtccgca tttgagcctt gttctggggc ccagcccaac acctggcttg 3060
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<210> 175

<211> 636

<212> PRT

<213> Homo sapiens

<220>

<221> MOD\_RES

<222> (539)

<223> Any amino acid

<400> 175

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Met Thr Thr Trp Ser Leu Arg Arg Arg Pro Ala Arg Thr Leu Gly Leu
 1              5              10              15

```

```

Leu Leu Leu Val Val Leu Gly Phe Leu Val Leu Arg Arg Leu Asp Trp
      20              25              30

```

```

Ser Thr Leu Val Pro Leu Arg Leu Arg His Arg Gln Leu Gly Leu Gln
      35              40              45

```

```

Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp Ile Phe
      50              55              60

```

```

Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp Arg Asp
      65              70              75              80

```

```

Arg Leu Leu Lys Met Lys Ala Cys Gly Leu Asn Thr Leu Thr Thr Tyr
      85              90              95

```

```

Val Pro Trp Asn Leu His Glu Pro Glu Arg Gly Lys Phe Asp Phe Ser
      100             105             110

```

```

Gly Asn Leu Asp Leu Glu Ala Phe Val Leu Met Ala Ala Glu Ile Gly
      115             120             125

```

```

Leu Trp Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ser Glu Met Asp
      130             135             140

```

09905056.07.1204

|            |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu<br>145 | Gly | Gly | Leu | Pro | Ser | Trp | Leu | Leu | Gln | Asp | Pro | Gly | Met | Arg | Leu |
|            |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Arg        | Thr | Thr | Tyr | Lys | Gly | Phe | Thr | Glu | Ala | Val | Asp | Leu | Tyr | Phe | Asp |
|            |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| His        | Leu | Met | Ser | Arg | Val | Val | Pro | Leu | Gln | Tyr | Lys | Arg | Gly | Gly | Pro |
|            |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ile        | Ile | Ala | Val | Gln | Val | Glu | Asn | Glu | Tyr | Gly | Ser | Tyr | Asn | Lys | Asp |
|            |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Pro        | Ala | Tyr | Met | Pro | Tyr | Val | Lys | Lys | Ala | Leu | Glu | Asp | Arg | Gly | Ile |
|            | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Val        | Glu | Leu | Leu | Leu | Thr | Ser | Asp | Asn | Lys | Asp | Gly | Leu | Ser | Lys | Gly |
| 225        |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Ile        | Val | Gln | Gly | Val | Leu | Ala | Thr | Ile | Asn | Leu | Gln | Ser | Thr | His | Glu |
|            |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Leu        | Gln | Leu | Leu | Thr | Thr | Phe | Leu | Phe | Asn | Val | Gln | Gly | Thr | Gln | Pro |
|            |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Lys        | Met | Val | Met | Glu | Tyr | Trp | Thr | Gly | Trp | Phe | Asp | Ser | Trp | Gly | Gly |
|            |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Pro        | His | Asn | Ile | Leu | Asp | Ser | Ser | Glu | Val | Leu | Lys | Thr | Val | Ser | Ala |
|            | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ile        | Val | Asp | Ala | Gly | Ser | Ser | Ile | Asn | Leu | Tyr | Met | Phe | His | Gly | Gly |
| 305        |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Thr        | Asn | Phe | Gly | Phe | Met | Asn | Gly | Ala | Met | His | Phe | His | Asp | Tyr | Lys |
|            |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Ser        | Asp | Val | Thr | Ser | Tyr | Asp | Tyr | Asp | Ala | Val | Leu | Thr | Glu | Ala | Gly |
|            |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Asp        | Tyr | Thr | Ala | Lys | Tyr | Met | Lys | Leu | Arg | Asp | Phe | Phe | Gly | Ser | Ile |
|            |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Ser        | Gly | Ile | Pro | Leu | Pro | Pro | Pro | Pro | Asp | Leu | Leu | Pro | Lys | Met | Pro |
|            | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Tyr        | Glu | Pro | Leu | Thr | Pro | Val | Leu | Tyr | Leu | Ser | Leu | Trp | Asp | Ala | Leu |
| 385        |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Lys        | Tyr | Leu | Gly | Glu | Pro | Ile | Lys | Ser | Glu | Lys | Pro | Ile | Asn | Met | Glu |
|            |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Asn        | Leu | Pro | Val | Asn | Gly | Gly | Asn | Gly | Gln | Ser | Phe | Gly | Tyr | Ile | Leu |
|            |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |

Tyr Glu Thr Ser Ile Thr Ser Ser Gly Ile Leu Ser Gly His Val His  
435 440 445

Asp Arg Gly Gln Val Phe Val Asn Thr Val Ser Ile Gly Phe Leu Asp  
450 455 460

Tyr Lys Thr Thr Lys Ile Ala Val Pro Leu Ile Gln Gly Tyr Thr Val  
465 470 475 480

Leu Arg Ile Leu Val Glu Asn Arg Gly Arg Val Asn Tyr Gly Glu Asn  
485 490 495

Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu Asn Asp  
500 505 510

Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met Lys Lys Ser  
515 520 525

Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Xaa Ser Leu Pro Glu Thr  
530 535 540

Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu Ser Ile Ser Ser Thr  
545 550 555 560

Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly Trp Glu Lys Gly Val Val  
565 570 575

Phe Ile Asn Gly Gln Asn Leu Gly Arg Tyr Trp Asn Ile Gly Pro Gln  
580 585 590

Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile Asn Gln  
595 600 605

Val Ile Val Phe Glu Glu Thr Met Ala Gly Pro Ala Leu Gln Phe Thr  
610 615 620

Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys  
625 630 635

<210> 176

<211> 2505

<212> DNA

<213> Homo sapiens

<400> 176

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aaggggagca aagccgggct cggcccaggg cccccaggac ctccatctcc caatgttgga 180  
ggaatccgac acgtgacggg ctgtccgcgg tctcagacta gaggagcgct gtaaacgcca 240  
tggtctccaa gaagctgtcc tgccttcggt ccctgctgct gccgctcagc ctgacgctac 300  
tgctgcccc a ggcagacact cggtcgttcg tagtggatag gggtcatgac cggtttctcc 360  
tagacggggc cccgttcgcg tatgtgtctg gcagcctgca ctactttcgg gtaccgcggg 420

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 ggaccaaggg ccaagtctgg atcaatgggt ttaacttggg ccggtactgg acaaagcagg 1980  
 ggccacaaca gacctctac gtgccaagat tctgtctgtt tcctagggga gccctcaaca 2040  
 aaattacatt gctggaacta gaagatgtac ctctccagcc ccaagtccaa tttttggata 2100  
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<210> 177

<211> 654

<212> PRT

<213> Homo sapiens

<400> 177

Met Ala Pro Lys Lys Leu Ser Cys Leu Arg Ser Leu Leu Leu Pro Leu  
 1 5 10 15

Ser Leu Thr Leu Leu Leu Pro Gln Ala Asp Thr Arg Ser Phe Val Val  
 20 25 30

Asp Arg Gly His Asp Arg Phe Leu Leu Asp Gly Ala Pro Phe Arg Tyr  
 35 40 45

Val Ser Gly Ser Leu His Tyr Phe Arg Val Pro Arg Val Leu Trp Ala  
 50 55 60

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Arg | Leu | Leu | Lys | Met | Arg | Trp | Ser | Gly | Leu | Asn | Ala | Ile | Gln | Phe | 65  | 70  | 75  | 80  |
| Tyr | Val | Pro | Trp | Asn | Tyr | His | Glu | Pro | Gln | Pro | Gly | Val | Tyr | Asn | Phe | 85  | 90  | 95  |     |
| Asn | Gly | Ser | Arg | Asp | Leu | Ile | Ala | Phe | Leu | Asn | Glu | Ala | Ala | Leu | Ala | 100 | 105 | 110 |     |
| Asn | Leu | Leu | Val | Ile | Leu | Arg | Pro | Gly | Pro | Tyr | Ile | Cys | Ala | Glu | Trp | 115 | 120 | 125 |     |
| Glu | Met | Gly | Gly | Leu | Pro | Ser | Trp | Leu | Leu | Arg | Lys | Pro | Glu | Ile | His | 130 | 135 | 140 |     |
| Leu | Arg | Thr | Ser | Asp | Pro | Asp | Phe | Leu | Ala | Ala | Val | Asp | Ser | Trp | Phe | 145 | 150 | 155 | 160 |
| Lys | Val | Leu | Leu | Pro | Lys | Ile | Tyr | Pro | Trp | Leu | Tyr | His | Asn | Gly | Gly | 165 | 170 | 175 |     |
| Asn | Ile | Ile | Ser | Ile | Gln | Val | Glu | Asn | Glu | Tyr | Gly | Ser | Tyr | Arg | Ala | 180 | 185 | 190 |     |
| Cys | Asp | Phe | Ser | Tyr | Met | Arg | His | Leu | Ala | Gly | Leu | Phe | Arg | Ala | Leu | 195 | 200 | 205 |     |
| Leu | Gly | Glu | Lys | Ile | Leu | Leu | Phe | Thr | Thr | Asp | Gly | Pro | Glu | Gly | Leu | 210 | 215 | 220 |     |
| Lys | Cys | Gly | Ser | Leu | Arg | Gly | Leu | Tyr | Thr | Thr | Val | Asp | Phe | Gly | Pro | 225 | 230 | 235 | 240 |
| Ala | Asp | Asn | Met | Thr | Lys | Ile | Phe | Thr | Leu | Leu | Arg | Lys | Tyr | Glu | Pro | 245 | 250 | 255 |     |
| His | Gly | Pro | Leu | Val | Asn | Ser | Glu | Tyr | Tyr | Thr | Gly | Trp | Leu | Asp | Tyr | 260 | 265 | 270 |     |
| Trp | Gly | Gln | Asn | His | Ser | Thr | Arg | Ser | Val | Ser | Ala | Val | Thr | Lys | Gly | 275 | 280 | 285 |     |
| Leu | Glu | Asn | Met | Leu | Lys | Leu | Gly | Ala | Ser | Val | Asn | Met | Tyr | Met | Phe | 290 | 295 | 300 |     |
| His | Gly | Gly | Thr | Asn | Phe | Gly | Tyr | Trp | Asn | Gly | Ala | Asp | Lys | Lys | Gly | 305 | 310 | 315 | 320 |
| Arg | Phe | Leu | Pro | Ile | Thr | Thr | Ser | Tyr | Asp | Tyr | Asp | Ala | Pro | Ile | Ser | 325 | 330 | 335 |     |
| Glu | Ala | Gly | Asp | Pro | Thr | Pro | Lys | Leu | Phe | Ala | Leu | Arg | Asp | Val | Ile |     |     |     |     |

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|   |     |     |
|---|-----|-----|
| 340   | 345 | 350 |
| Ser Lys Phe Gln Glu Val Pro Leu Gly Pro Leu Pro Pro Pro Ser Pro |     |     |
| 355   | 360 | 365 |
| Lys Met Met Leu Gly Pro Val Thr Leu His Leu Val Gly His Leu Leu |     |     |
| 370   | 375 | 380 |
| Ala Phe Leu Asp Leu Leu Cys Pro Arg Gly Pro Ile His Ser Ile Leu |     |     |
| 385   | 390 | 395 |
| Pro Met Thr Phe Glu Ala Val Lys Gln Asp His Gly Phe Met Leu Tyr |     |     |
| 405   | 410 | 415 |
| Arg Thr Tyr Met Thr His Thr Ile Phe Glu Pro Thr Pro Phe Trp Val |     |     |
| 420   | 425 | 430 |
| Pro Asn Asn Gly Val His Asp Arg Ala Tyr Val Met Val Asp Gly Val |     |     |
| 435   | 440 | 445 |
| Phe Gln Gly Val Val Glu Arg Asn Met Arg Asp Lys Leu Phe Leu Thr |     |     |
| 450   | 455 | 460 |
| Gly Lys Leu Gly Ser Lys Leu Asp Ile Leu Val Glu Asn Met Gly Arg |     |     |
| 465   | 470 | 475 |
| Leu Ser Phe Gly Ser Asn Ser Ser Asp Phe Lys Gly Leu Leu Lys Pro |     |     |
| 485   | 490 | 495 |
| Pro Ile Leu Gly Gln Thr Ile Leu Thr Gln Trp Met Met Phe Pro Leu |     |     |
| 500   | 505 | 510 |
| Lys Ile Asp Asn Leu Val Lys Trp Trp Phe Pro Leu Gln Leu Pro Lys |     |     |
| 515   | 520 | 525 |
| Trp Pro Tyr Pro Gln Ala Pro Ser Gly Pro Thr Phe Tyr Ser Lys Thr |     |     |
| 530   | 535 | 540 |
| Phe Pro Ile Leu Gly Ser Val Gly Asp Thr Phe Leu Tyr Leu Pro Gly |     |     |
| 545   | 550 | 555 |
| Trp Thr Lys Gly Gln Val Trp Ile Asn Gly Phe Asn Leu Gly Arg Tyr |     |     |
| 565   | 570 | 575 |
| Trp Thr Lys Gln Gly Pro Gln Gln Thr Leu Tyr Val Pro Arg Phe Leu |     |     |
| 580   | 585 | 590 |
| Leu Phe Pro Arg Gly Ala Leu Asn Lys Ile Thr Leu Leu Glu Leu Glu |     |     |
| 595   | 600 | 605 |
| Asp Val Pro Leu Gln Pro Gln Val Gln Phe Leu Asp Lys Pro Ile Leu |     |     |
| 610   | 615 | 620 |

Asp Thr Leu Ser Ala Ser Glu Pro Met Glu Leu Ser Gly His  
645 650

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<210> 178
<211> 24
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 178  
tggctactcc aagacctgg catg 24

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<210> 179
<211> 24
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 179  
tggacaaatc cccttqctca gcc 24

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<210> 180
<211> 50
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 180  
gggtcttcacc gaagcagtgg acctttattt tgaccacctg atgtccaggg 50

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<210> 181
<211> 22
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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<400> 181
ccagctatga ctatgatgca cc                22
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| gcacccacaa | tatggcttac  | atgttgaaaa  | agctttctcat | cagttacata | tccattatatt | 120  |  |
| gtgtttatgg | ctttatctgc  | ctctacactc  | tcttctgggt  | attcaggata | cctttgaagg  | 180  |  |
| aatattcttt | cgaaaaagtc  | agagaagaga  | gcagtttttag | tgacattcca | gatgtcaaaa  | 240  |  |
| acgattttgc | gttccttctt  | cacatggtag  | accagtatga  | ccagctatat | tccaagcgtt  | 300  |  |
| ttggtgtgtt | cttgtcagaa  | gttagtgaaa  | ataaacttag  | ggaaatttag | ttgaaccatg  | 360  |  |
| agtggacatt | tgaaaaactc  | aggcagcaca  | tttcacgc aa | cgccaggac  | aagcaggagt  | 420  |  |
| tgcattctgt | catgctgtcg  | ggggtgcccg  | atgtgtctct  | tgacctcaca | gacctggatg  | 480  |  |
| tgctaaagct | tgaactaatt  | ccagaagcta  | aaattcctgc  | taagatttct | caaatgacta  | 540  |  |
| acctccaaga | gtccacctc   | tgcactgcc   | ctgcaaaagt  | tgaacagact | gcttttagct  | 600  |  |
| ttcttcgcga | tcacttgaga  | tgccttcacg  | tgaagttcac  | tgatgtggct | gaaattcctg  | 660  |  |
| cctgggtgta | tttgctcaaa  | aaccttcgag  | agttgtactt  | aataggcaat | ttgaactctg  | 720  |  |
| aaaacaataa | gatgatagga  | cttgaatctc  | tccgagagtt  | gcggcacctt | aagattctcc  | 780  |  |
| acgtgaagag | caatttgacc  | aaagtccct   | ccaacattac  | agatgtggct | ccacatctta  | 840  |  |
| caaagttagt | cattcataat  | gacggcacta  | aactcttggt  | actgaacagc | cttaagaaaa  | 900  |  |
| tgatgaatgt | cgctgagctg  | gaactccaga  | actgtgagct  | agagagaatc | ccacatgcta  | 960  |  |
| ttttcagcct | ctctaattta  | caggaaactgg | atttaaagtc  | caataacatt | cgcacaattg  | 1020 |  |
| aggaaatcat | cagtttccag  | catttaaaac  | gactgacttg  | tttaaaatta | tggcataaca  | 1080 |  |
| aaattgttac | tattctctcc  | tctattacc   | atgtcaaaaa  | cttggagtca | ctttatttct  | 1140 |  |
| ctaacaacaa | gctcgaatcc  | ttaccagtgg  | cagtatttag  | ttacagaaa  | ctcagatgct  | 1200 |  |
| tagatgtgag | ctacaacaac  | atttcaatga  | ttccaataga  | aataggattg | cttcagaacc  | 1260 |  |
| tgcagcattt | gcataatcact | gggaacaaaq  | tqqacattct  | qccaaaacaa | ttgtttaaat  | 1320 |  |

gcataaagtt gaggactttg aatctgggac agaactgcat cacctcactc ccagagaaaag 1380  
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 cagcccagct gggccagtgt cggatgctca agaaaagcgg gcttggttgga gaagatcacc 1500  
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 ttgcaaattgg gattttaaact aagataatat atgcacagtg atgtgcagga acaacttcct 1620  
 agattgcaag tgctcacgta caagttatta caagataatg catttttagga gtagatacat 1680  
 ctttttaaaat aaaacagaga ggatgcatag aaggctgata gaagacataa ctgaatgttc 1740  
 aatgttttga ggggttttaag tcattcattt ccaaatacatt tttttttttc ttttggggaa 1800  
 agggaaggaa aaattataat cactaatctt gggtcttttt aaattgtttg taacttggat 1860  
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<210> 185

<211> 501

<212> PRT

<213> Homo sapiens

<400> 185

Met Ala Tyr Met Leu Lys Lys Leu Leu Ile Ser Tyr Ile Ser Ile Ile  
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 20 25 30

Ile Pro Leu Lys Glu Tyr Ser Phe Glu Lys Val Arg Glu Glu Ser Ser  
 35 40 45

Phe Ser Asp Ile Pro Asp Val Lys Asn Asp Phe Ala Phe Leu Leu His  
 50 55 60

Met Val Asp Gln Tyr Asp Gln Leu Tyr Ser Lys Arg Phe Gly Val Phe  
 65 70 75 80

Leu Ser Glu Val Ser Glu Asn Lys Leu Arg Glu Ile Ser Leu Asn His  
 85 90 95

Glu Trp Thr Phe Glu Lys Leu Arg Gln His Ile Ser Arg Asn Ala Gln  
 100 105 110

Asp Lys Gln Glu Leu His Leu Phe Met Leu Ser Gly Val Pro Asp Ala  
 115 120 125

Val Phe Asp Leu Thr Asp Leu Asp Val Leu Lys Leu Glu Leu Ile Pro  
 130 135 140

Glu Ala Lys Ile Pro Ala Lys Ile Ser Gln Met Thr Asn Leu Gln Glu  
 145 150 155 160

Leu His Leu Cys His Cys Pro Ala Lys Val Glu Gln Thr Ala Phe Ser  
 165 170 175

Phe Leu Arg Asp His Leu Arg Cys Leu His Val Lys Phe Thr Asp Val  
 180 185 190

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Ala Glu Ile Pro Ala Trp Val Tyr Leu Leu Lys Asn Leu Arg Glu Leu  
 195 200 205  
 Tyr Leu Ile Gly Asn Leu Asn Ser Glu Asn Asn Lys Met Ile Gly Leu  
 210 215 220  
 Glu Ser Leu Arg Glu Leu Arg His Leu Lys Ile Leu His Val Lys Ser  
 225 230 235 240  
 Asn Leu Thr Lys Val Pro Ser Asn Ile Thr Asp Val Ala Pro His Leu  
 245 250 255  
 Thr Lys Leu Val Ile His Asn Asp Gly Thr Lys Leu Leu Val Leu Asn  
 260 265 270  
 Ser Leu Lys Lys Met Met Asn Val Ala Glu Leu Glu Leu Gln Asn Cys  
 275 280 285  
 Glu Leu Glu Arg Ile Pro His Ala Ile Phe Ser Leu Ser Asn Leu Gln  
 290 295 300  
 Glu Leu Asp Leu Lys Ser Asn Asn Ile Arg Thr Ile Glu Glu Ile Ile  
 305 310 315 320  
 Ser Phe Gln His Leu Lys Arg Leu Thr Cys Leu Lys Leu Trp His Asn  
 325 330 335  
 Lys Ile Val Thr Ile Pro Pro Ser Ile Thr His Val Lys Asn Leu Glu  
 340 345 350  
 Ser Leu Tyr Phe Ser Asn Asn Lys Leu Glu Ser Leu Pro Val Ala Val  
 355 360 365  
 Phe Ser Leu Gln Lys Leu Arg Cys Leu Asp Val Ser Tyr Asn Asn Ile  
 370 375 380  
 Ser Met Ile Pro Ile Glu Ile Gly Leu Leu Gln Asn Leu Gln His Leu  
 385 390 395 400  
 His Ile Thr Gly Asn Lys Val Asp Ile Leu Pro Lys Gln Leu Phe Lys  
 405 410 415  
 Cys Ile Lys Leu Arg Thr Leu Asn Leu Gly Gln Asn Cys Ile Thr Ser  
 420 425 430  
 Leu Pro Glu Lys Val Gly Gln Leu Ser Gln Leu Thr Gln Leu Glu Leu  
 435 440 445  
 Lys Gly Asn Cys Leu Asp Arg Leu Pro Ala Gln Leu Gly Gln Cys Arg  
 450 455 460  
 Met Leu Lys Lys Ser Gly Leu Val Val Glu Asp His Leu Phe Asp Thr

0905056.07201  
 0905056.07201

|   |   |     |     |
|---|---|-----|-----|
| 465   | 470   | 475 | 480 |
| Leu Pro Leu Glu Val Lys Glu Ala Leu Asn Gln Asp Ile Asn Ile Pro       |   |     |     |
|   | 485   | 490 | 495 |
| Phe Ala Asn Gly Ile   |   |     |     |
| 500   |   |     |     |
| <br>  |   |     |     |
| <210>   | 186   |     |     |
| <211>   | 21  |     |     |
| <212>   | DNA   |     |     |
| <213>   | Artificial Sequence   |     |     |
| <br>  |   |     |     |
| <220>   |   |     |     |
| <223>   | Description of Artificial Sequence: Synthetic oligonucleotide probe |     |     |
| <br>  |   |     |     |
| <400>   | 186   |     |     |
| cctccctcta ttacccatgt c   |   |     | 21  |
| <br>  |   |     |     |
| <210>   | 187   |     |     |
| <211>   | 24  |     |     |
| <212>   | DNA   |     |     |
| <213>   | Artificial Sequence   |     |     |
| <br>  |   |     |     |
| <220>   |   |     |     |
| <223>   | Description of Artificial Sequence: Synthetic oligonucleotide probe |     |     |
| <br>  |   |     |     |
| <400>   | 187   |     |     |
| gaccaacttt ctctgggagt gagg  |   |     | 24  |
| <br>  |   |     |     |
| <210>   | 188   |     |     |
| <211>   | 47  |     |     |
| <212>   | DNA   |     |     |
| <213>   | Artificial Sequence   |     |     |
| <br>  |   |     |     |
| <220>   |   |     |     |
| <223>   | Description of Artificial Sequence: Synthetic oligonucleotide probe |     |     |
| <br>  |   |     |     |
| <400>   | 188   |     |     |
| gtcactttat ttctctaaca acaagctcga atccttacca gtggcag                   |   |     | 47  |
| <br>  |   |     |     |
| <210>   | 189   |     |     |
| <211>   | 2917  |     |     |
| <212>   | DNA   |     |     |
| <213>   | Homo sapiens  |     |     |
| <br>  |   |     |     |
| <400>   | 189   |     |     |
| cccacgcgtc cggccttctc tctggacttt gcatttccat tccttttcat tgacaaactg 60  |   |     |     |
| acttttttta tttctttttt tccatctctg ggccagcttg ggatcctagg ccgccctggg 120 |   |     |     |
| aagacatttg tgttttacac acataaggat ctgtgtttgg qgtttcttct tcctccctg 180  |   |     |     |

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 cacaacccag acaaggtgtg gtgggccaag aacagccagg ccaaaaccat tgccacggag 480  
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 gcagagccct gaagacttca atgatgtcaa tgaggccacc tgtttgtgat gtgcaggcac 660  
 agaagaaagg cacagctccc catcagtttc atggaaaata actcagtgcc tgctgggaac 720  
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 ggggagagag aacctcact gtggggaatg ctgataaacc agtcacacag ctgctctatt 840  
 ctcacacaaa tctacctctt gcgtggctgg aactgacgtt tccctggagg tgtccagaaa 900  
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 gatacctgta gagcctctcc cacctctgac tttgcatctc caacctacga cctaatacaag 2340  
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 ttccagttta atgcctttaa attcttgaga agtatgagct ctgtgtatct gcagtgtaaa 2460  
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 gaaactccaa accagccttt caacagtgtg catctgtttt ccttcatggg tctagctctg 2700  
 aatgtggtga ctgtagcgac aatcacagtg aggcattttg taaatcaacg ggcagactac 2760  
 aaataccaga agctgcagaa ctattaacta acagggtcaa ccctaagtga gacatgtttc 2820  
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&lt;210&gt; 190

&lt;211&gt; 607

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 190

Met Glu Leu Val Arg Arg Leu Met Pro Leu Thr Leu Leu Ile Leu Ser  
 1 5 10 15  
 Cys Leu Ala Glu Leu Thr Met Ala Glu Ala Glu Gly Asn Ala Ser Cys  
 20 25 30  
 Thr Val Ser Leu Gly Gly Ala Asn Met Ala Glu Thr His Lys Ala Met  
 35 40 45  
 Ile Leu Gln Leu Asn Pro Ser Glu Asn Cys Thr Trp Thr Ile Glu Arg  
 50 55 60  
 Pro Glu Asn Lys Ser Ile Arg Ile Ile Phe Ser Tyr Val Gln Leu Asp  
 65 70 75 80  
 Pro Asp Gly Ser Cys Glu Ser Glu Asn Ile Lys Val Phe Asp Gly Thr  
 85 90 95  
 Ser Ser Asn Gly Pro Leu Leu Gly Gln Val Cys Ser Lys Asn Asp Tyr  
 100 105 110  
 Val Pro Val Phe Glu Ser Ser Ser Ser Thr Leu Thr Phe Gln Ile Val  
 115 120 125  
 Thr Asp Ser Ala Arg Ile Gln Arg Thr Val Phe Val Phe Tyr Tyr Phe  
 130 135 140  
 Phe Ser Pro Asn Ile Ser Ile Pro Asn Cys Gly Gly Tyr Leu Asp Thr  
 145 150 155 160  
 Leu Glu Gly Ser Phe Thr Ser Pro Asn Tyr Pro Lys Pro His Pro Glu  
 165 170 175  
 Leu Ala Tyr Cys Val Trp His Ile Gln Val Glu Lys Asp Tyr Lys Ile  
 180 185 190  
 Lys Leu Asn Phe Lys Glu Ile Phe Leu Glu Ile Asp Lys Gln Cys Lys  
 195 200 205  
 Phe Asp Phe Leu Ala Ile Tyr Asp Gly Pro Ser Thr Asn Ser Gly Leu  
 210 215 220  
 Ile Gly Gln Val Cys Gly Arg Val Thr Pro Thr Phe Glu Ser Ser Ser  
 225 230 235 240  
 Asn Ser Leu Thr Val Val Leu Ser Thr Asp Tyr Ala Asn Ser Tyr Arg  
 245 250 255  
 Gly Phe Ser Ala Ser Tyr Thr Ser Ile Tyr Ala Glu Asn Ile Asn Thr  
 260 265 270  
 Thr Ser Leu Thr Cys Ser Ser Asp Arg Met Arg Val Ile Ile Ser Lys  
 275 280 285

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 T03T20 9505000

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Tyr | Leu | Glu | Ala | Phe | Asn | Ser | Asn | Gly | Asn | Asn | Leu | Gln | Leu | Lys |
| 290 |     |     |     |     |     | 295 |     |     |     | 300 |     |     |     |     |     |
| Asp | Pro | Thr | Cys | Arg | Pro | Lys | Leu | Ser | Asn | Val | Val | Glu | Phe | Ser | Val |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Pro | Leu | Asn | Gly | Cys | Gly | Thr | Ile | Arg | Lys | Val | Glu | Asp | Gln | Ser | Ile |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Thr | Tyr | Thr | Asn | Ile | Ile | Thr | Phe | Ser | Ala | Ser | Ser | Thr | Ser | Glu | Val |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Ile | Thr | Arg | Gln | Lys | Gln | Leu | Gln | Ile | Ile | Val | Lys | Cys | Glu | Met | Gly |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| His | Asn | Ser | Thr | Val | Glu | Ile | Ile | Tyr | Ile | Thr | Glu | Asp | Asp | Val | Ile |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Gln | Ser | Gln | Asn | Ala | Leu | Gly | Lys | Tyr | Asn | Thr | Ser | Met | Ala | Leu | Phe |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Glu | Ser | Asn | Ser | Phe | Glu | Lys | Thr | Ile | Leu | Glu | Ser | Pro | Tyr | Tyr | Val |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Asp | Leu | Asn | Gln | Thr | Leu | Phe | Val | Gln | Val | Ser | Leu | His | Thr | Ser | Asp |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Pro | Asn | Leu | Val | Val | Phe | Leu | Asp | Thr | Cys | Arg | Ala | Ser | Pro | Thr | Ser |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Asp | Phe | Ala | Ser | Pro | Thr | Tyr | Asp | Leu | Ile | Lys | Ser | Gly | Cys | Ser | Arg |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Asp | Glu | Thr | Cys | Lys | Val | Tyr | Pro | Leu | Phe | Gly | His | Tyr | Gly | Arg | Phe |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |
| Gln | Phe | Asn | Ala | Phe | Lys | Phe | Leu | Arg | Ser | Met | Ser | Ser | Val | Tyr | Leu |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |
| Gln | Cys | Lys | Val | Leu | Ile | Cys | Asp | Ser | Ser | Asp | His | Gln | Ser | Arg | Cys |
|     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |
| Asn | Gln | Gly | Cys | Val | Ser | Arg | Ser | Lys | Arg | Asp | Ile | Ser | Ser | Tyr | Lys |
|     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |
| Trp | Lys | Thr | Asp | Ser | Ile | Ile | Gly | Pro | Ile | Arg | Leu | Lys | Arg | Asp | Arg |
|     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |
| Ser | Ala | Ser | Gly | Asn | Ser | Gly | Phe | Gln | His | Glu | Thr | His | Ala | Glu | Glu |
| 545 |     |     |     |     | 550 |     |     |     |     | 555 |     |     |     |     | 560 |
| Thr | Pro | Asn | Gln | Pro | Phe | Asn | Ser | Val | His | Leu | Phe | Ser | Phe | Met | Val |

565

570

575

Leu Ala Leu Asn Val Val Thr Val Ala Thr Ile Thr Val Arg His Phe  
                   580                                  585                                  590

Val Asn Gln Arg Ala Asp Tyr Lys Tyr Gln Lys Leu Gln Asn Tyr  
                   595                                  600                                  605

&lt;210&gt; 191

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 191

tctctattcc aaactgtggc g

21

&lt;210&gt; 192

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 192

tttgatgacg attcgaaggt gg

22

&lt;210&gt; 193

&lt;211&gt; 47

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 193

ggaaggatcc ttcaccagcc ccaattaccc aaagccgcac cctgagc

47

&lt;210&gt; 194

&lt;211&gt; 2362

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 194

gacggaagaa cagcgctccc gaggccgcgg gagcctgcag agaggacagc cggcctgcgc 60  
 cgggacatgc ggccccagga gctccccagg ctgcggttcc cggttgctgct gttgctgttg 120  
 ctgctgctgc cgccgcgcgc gtgcctgcgc cacagcgcca cgcgcttcga cccacactgg 180

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 aactatcagc ctgaggttct gtggtcggat ggtgacggag gagcaccgga tcaatactgg 780  
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 accaatgacg gttggggagc tggtagcctg tgaagcatg gtggcttcta tacctgcagt 900  
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 gcaacagagg tgaaactact gggccatgga cagccactta actggatttc tttggagcaa 1380  
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 tatatagtta tgcatactt aatatgggga tattttctgg gaaatgcatt gctagtcaat 1860  
 ttttttttgt gccaacatca tagagtgtat ttacaaaatc ctagatggca tagcctacta 1920  
 cacaccta atgtgtatggta tagactgttg ctctaggct acagacatat acagcatgtt 1980  
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 taggacatta ttgaacactg ccagacgtta taaatactgt atgcttaggc tacactacat 2220  
 ttataaaaaa aagtttttct ttcttcaatt ataaattaac ataagtgtac tgtaacttta 2280  
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 taaactcatt gtgcaaatgt aa 2362

<210> 195

<211> 467

<212> PRT

<213> Homo sapiens

<400> 195

Met Arg Pro Gln Glu Leu Pro Arg Leu Ala Phe Pro Leu Leu Leu Leu  
 1 5 10 15

Leu Leu Leu Leu Leu Pro Pro Pro Pro Cys Pro Ala His Ser Ala Thr  
 20 25 30

Arg Phe Asp Pro Thr Trp Glu Ser Leu Asp Ala Arg Gln Leu Pro Ala  
 35 40 45

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Phe | Asp | Gln | Ala | Lys | Phe | Gly | Ile | Phe | Ile | His | Trp | Gly | Val | Phe |
| 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Val | Pro | Ser | Phe | Gly | Ser | Glu | Trp | Phe | Trp | Trp | Tyr | Trp | Gln | Lys |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Glu | Lys | Ile | Pro | Lys | Tyr | Val | Glu | Phe | Met | Lys | Asp | Asn | Tyr | Pro | Pro |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Phe | Lys | Tyr | Glu | Asp | Phe | Gly | Pro | Leu | Phe | Thr | Ala | Lys | Phe | Phe |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asn | Ala | Asn | Gln | Trp | Ala | Asp | Ile | Phe | Gln | Ala | Ser | Gly | Ala | Lys | Tyr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Val | Leu | Thr | Ser | Lys | His | His | Glu | Gly | Phe | Thr | Leu | Trp | Gly | Ser |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Glu | Tyr | Ser | Trp | Asn | Trp | Asn | Ala | Ile | Asp | Glu | Gly | Pro | Lys | Arg | Asp |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ile | Val | Lys | Glu | Leu | Glu | Val | Ala | Ile | Arg | Asn | Arg | Thr | Asp | Leu | Arg |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Phe | Gly | Leu | Tyr | Tyr | Ser | Leu | Phe | Glu | Trp | Phe | His | Pro | Leu | Phe | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Glu | Asp | Glu | Ser | Ser | Ser | Phe | His | Lys | Arg | Gln | Phe | Pro | Val | Ser | Lys |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Thr | Leu | Pro | Glu | Leu | Tyr | Glu | Leu | Val | Asn | Asn | Tyr | Gln | Pro | Glu | Val |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Leu | Trp | Ser | Asp | Gly | Asp | Gly | Gly | Ala | Pro | Asp | Gln | Tyr | Trp | Asn | Ser |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Thr | Gly | Phe | Leu | Ala | Trp | Leu | Tyr | Asn | Glu | Ser | Pro | Val | Arg | Gly | Thr |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Val | Val | Thr | Asn | Asp | Arg | Trp | Gly | Ala | Gly | Ser | Ile | Cys | Lys | His | Gly |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Gly | Phe | Tyr | Thr | Cys | Ser | Asp | Arg | Tyr | Asn | Pro | Gly | His | Leu | Leu | Pro |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| His | Lys | Trp | Glu | Asn | Cys | Met | Thr | Ile | Asp | Lys | Leu | Ser | Trp | Gly | Tyr |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Arg | Arg | Glu | Ala | Gly | Ile | Ser | Asp | Tyr | Leu | Thr | Ile | Glu | Glu | Leu | Val |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Lys | Gln | Leu | Val | Glu | Thr | Val | Ser | Cys | Gly | Gly | Asn | Leu | Leu | Met | Asn |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |

Ile Gly Pro Thr Leu Asp Gly Thr Ile Ser Val Val Phe Glu Glu Arg  
 340 345 350

Leu Arg Gln Val Gly Ser Trp Leu Lys Val Asn Gly Glu Ala Ile Tyr  
 355 360 365

Glu Thr Tyr Thr Trp Arg Ser Gln Asn Asp Thr Val Thr Pro Asp Val  
 370 375 380

Trp Tyr Thr Ser Lys Pro Lys Glu Lys Leu Val Tyr Ala Ile Phe Leu  
 385 390 395 400

Lys Trp Pro Thr Ser Gly Gln Leu Phe Leu Gly His Pro Lys Ala Ile  
 405 410 415

Leu Gly Ala Thr Glu Val Lys Leu Leu Gly His Gly Gln Pro Leu Asn  
 420 425 430

Trp Ile Ser Leu Glu Gln Asn Gly Ile Met Val Glu Leu Pro Gln Leu  
 435 440 445

Thr Ile His Gln Met Pro Cys Lys Trp Gly Trp Ala Leu Ala Leu Thr  
 450 455 460

Asn Val Ile  
 465

<210> 196

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 196

tggtttgacc aggccaagtt cgg

23

<210> 197

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 197

ggattcatcc tcaaggaaga gcgg

24

<210> 198

<211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 198  
 aacttgccgc atcagccact ctgc 24

<210> 199  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 199  
 ttccgtgccc agcttcggta gcgagtgggt ctggtggtat tggca 45

<210> 200  
 <211> 2372  
 <212> DNA  
 <213> Homo sapiens

<400> 200  
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 gttccagaac tctccatccg gactagttat tgagcatctg cctctcatat caccagtggc 120  
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 gtgttgcttc tcacttccat ctggaccacg aggtcctctg tccaaggctc tttgcgtgca 240  
 gaagagcttt ccatccagggt gtcatgcaga attatgggga tcacccttgt gagcaaaaag 300  
 gcgaaccagc agctgaattt cacagaagct aaggaggcct gtaggctgct gggactaagt 360  
 ttggccggca aggaccaagt tgaaacagcc ttgaaagcta gctttgaaac ttgcagctat 420  
 ggctgggttg gagatggatt cgtggtcac tctaggatta gcccaaacc caagtgtggg 480  
 aaaaatgggg tgggtgtcct gatttgggaag gttccagtga gccgacagt tgcagcctat 540  
 tgttacaact catctgatac ttggactaac tcgtgcattc cagaaattat caccaccaa 600  
 gatcccatat tcaacactca aactgcaaca caaacaacag aatttattgt cagtgcagct 660  
 acctactcgg tggcatcccc ttactctaca ataactgccc ctactactac tctcctgct 720  
 ccagcttcca cttctattcc acggagaaaa aaattgattt gtgtcacaga agtttttatg 780  
 gaaactagca ccatgtctac agaaactgaa ccatttgttg aaaataaagc agcattcaag 840  
 aatgaagctg ctgggtttgg aggtgtcccc acggctctgc tagtgcttgc tctcctcttc 900  
 tttggtgctg cagctggctc tggattttgc tatgtcaaaa ggtatgtgaa ggccttcctc 960  
 tttacaaaaca agaatcagca gaaggaaatg atcgaaacca aagtagtaaa ggaggagaag 1020  
 gccaatgata gcaaccctaa tgaggaatca aagaaaactg ataaaaacc agaagagtcc 1080  
 aagagtccaa gcaaaactac cgtgcgatgc ctggaagctg aagtttagat gagacagaaa 1140  
 tgaggagaca cacctgaggc tggtttcttt catgctcctt accctgcccc agctggggaa 1200  
 atcaaaaggg ccaaagaacc aaagaagaaa gtccaccctt ggttcctaac tggaatcagc 1260  
 tcaggactgc cattggacta tggagtgcac caaagagaat gcccttctcc ttattgtaac 1320  
 cctgtctgga tcctatcctc ctacctccaa agcttccac gccctttcta gcctggctat 1380  
 gtccctaataa tatcccactg ggagaaagga gttttgcaaa gtgcaaggac ctaaaacatc 1440

```

tcatcagtat ccagtggtaa aaaggcctcc tggctgtctg aggetaggtg ggttgaaagc 1500
caaggagtca ctgagaccaa ggctttctct actgattccg cagctcagac cttttcttca 1560
gctctgaaag agaaacacgt atcccacctg acatgtcctt ctgagcccgg taagagcaaa 1620
agaatggcag aaaagtttag cccctgaaag ccatggagat tctcataact tgagacctaa 1680
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cactgttttag aacacacaca cttacttttt ctggtctcta ccactgctga ttttttctct 1860
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ttcaacaaac atttgctgaa tagctactat atgtcaagtg ctgtgcaagg tattacactc 2040
tgtaattgaa tattattcct caaaaaattg cacatagtag aacgctatct gggaagctat 2100
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gactaatctt attcattttc tctaatatgg caaccattat aaccttaatt tattattaac 2220
atacctaaga agtacattgt tacctctata taccaaagca cattttaaaa gtgccattaa 2280
caaatgtatc actagccctc ctttttccaa caagaaggga ctgagagatg cagaaatatt 2340
tgtgacaaaa aattaaagca tttagaaaac tt 2372

```

<210> 201

<211> 322

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic protein

<400> 201

```

Met Ala Arg Cys Phe Ser Leu Val Leu Leu Leu Thr Ser Ile Trp Thr
  1              5              10              15

```

```

Thr Arg Leu Leu Val Gln Gly Ser Leu Arg Ala Glu Glu Leu Ser Ile
      20              25              30

```

```

Gln Val Ser Cys Arg Ile Met Gly Ile Thr Leu Val Ser Lys Lys Ala
      35              40              45

```

```

Asn Gln Gln Leu Asn Phe Thr Glu Ala Lys Glu Ala Cys Arg Leu Leu
      50              55              60

```

```

Gly Leu Ser Leu Ala Gly Lys Asp Gln Val Glu Thr Ala Leu Lys Ala
      65              70              75              80

```

```

Ser Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly Asp Gly Phe Val Val
      85              90              95

```

```

Ile Ser Arg Ile Ser Pro Asn Pro Lys Cys Gly Lys Asn Gly Val Gly
      100              105              110

```

```

Val Leu Ile Trp Lys Val Pro Val Ser Arg Gln Phe Ala Ala Tyr Cys
      115              120              125

```

```

Tyr Asn Ser Ser Asp Thr Trp Thr Asn Ser Cys Ile Pro Glu Ile Ile
      130              135              140

```

Thr Thr Lys Asp Pro Ile Phe Asn Thr Gln Thr Ala Thr Gln Thr Thr  
 145 150 155 160  
 Glu Phe Ile Val Ser Asp Ser Thr Tyr Ser Val Ala Ser Pro Tyr Ser  
 165 170 175  
 Thr Ile Pro Ala Pro Thr Thr Thr Pro Pro Ala Pro Ala Ser Thr Ser  
 180 185 190  
 Ile Pro Arg Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu  
 195 200 205  
 Thr Ser Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala  
 210 215 220  
 Ala Phe Lys Asn Glu Ala Ala Gly Phe Gly Gly Val Pro Thr Ala Leu  
 225 230 235 240  
 Leu Val Leu Ala Leu Leu Phe Phe Gly Ala Ala Ala Gly Leu Gly Phe  
 245 250 255  
 Cys Tyr Val Lys Arg Tyr Val Lys Ala Phe Pro Phe Thr Asn Lys Asn  
 260 265 270  
 Gln Gln Lys Glu Met Ile Glu Thr Lys Val Val Lys Glu Glu Lys Ala  
 275 280 285  
 Asn Asp Ser Asn Pro Asn Glu Glu Ser Lys Lys Thr Asp Lys Asn Pro  
 290 295 300  
 Glu Glu Ser Lys Ser Pro Ser Lys Thr Thr Val Arg Cys Leu Glu Ala  
 305 310 315 320  
 Glu Val

<210> 202

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 202

gagctttcca tccaggtgtc atgc

24

<210> 203

<211> 22

<212> DNA

<213> Artificial Sequence



&lt;222&gt; (1003)

&lt;223&gt; a, t, c or g

&lt;400&gt; 206

```

agatggcggg cttggcacct ctaattgctc tcgtgtatcc ggtgccgcga ctttcacgat 60
ggctcgccca accttactac cttctgtcgg cctgtctctc tgctgccttc ctactcgtga 120
ggaaactgcc gccgctctgc cacggtctgc ccaccaacg cgaagacggg aaccctgtgt 180
actttgactg gagagaagtg gagatcctga tgtttctcag tgccattgtg atgatgaaga 240
accgcagatc catcactgtg gagcaacata taggcaacat tttcatgttt agtaaaaggg 300
ccaacacaat tcttttcttc cgcttgata ttgcgatggg cctactttac atcacactct 360
gcatagtgtt cctgatgacg tgcaaacccc ccctatatat gggccctgag tatatcaagt 420
acttcaatga taaaaccatt gatgaggaac tagaacggga caagagggtc acttggattg 480
tggaagtctt tgccaattgg tctaataact gccaatcatt tgcccctatc tatgctgacc 540
tctcccttaa atacaactgt acagggtctaa attttgggaa ggtggatgtt ggacgctata 600
ctgatgttag tacgcggtac aaagtgcgca catcacccct caccaagcaa ctccctacc 660
tgatcctgtt ccaagggtggc aaggaggcaa tgcggcggcc acagattgac aagaaaggac 720
gggctgtctc atggaccttc tctgaggaga atgtgatccg agaatttaac ttaaatgagc 780
tataccagcg ggccaagaaa ctatcaaagg ctggagacaa tatccctgag gacgagcctg 840
tggttcaac cccaccaca gtgtcagatg gggaaaacaa gaaggataaa taagatcctc 900
actttggcag tgccttctct cctgtcaatt ccaggctctt tccataacca caagcctgag 960
gctgcagcct ttnattnatg ttttcccttt ggctgngact ggntggggca gcatgcagct 1020
tctgatttta aagaggcatc tagggaattg tcaggcaccc tacaggaagg cctgccatgc 1080
tgtggccaac tgtttactg gagcaagaaa gagatctcat aggacggagg gggaaatggt 1140
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tttctccatg aaactctgtg gtttcatcat tccttcttag ttgacctgca cagcttggtt 1260
agacctagat ttaaccctaa ggtaagatgc tgggggtatag aacgctaaga attttcccc 1320
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gcctaacttt gtcgctagtc ctaaggagaa acctttaacc acaaagtttt tatcattgaa 1440
gacaatattg aacaaccccc tattttgtgg ggattgagaa ggggtgaata gaggcttgag 1500
actttccttt gtgtggtagg acttggagga gaaatccctt ggactttcac taacctctg 1560
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```

&lt;210&gt; 207

&lt;211&gt; 296

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 207

```

Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg
 1             5             10             15

Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu
 20             25             30

Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly
 35             40             45

Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg
 50             55             60

Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn
 65             70             75             80

```

0905056 071204



Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile Phe Met Phe  
85 90 95

Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp Ile Arg Met  
100 105 110

Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe Leu Met Thr Cys Lys  
115 120 125

Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Lys Tyr Phe Asn Asp Lys  
130 135 140

Thr Ile Asp Glu Glu Leu Glu Arg Asp Lys Arg Val Thr Trp Ile Val  
145 150 155 160

Glu Phe Phe Ala Asn Trp Ser Asn Asp Cys Gln Ser Phe Ala Pro Ile  
165 170 175

Tyr Ala Asp Leu Ser Leu Lys Tyr Asn Cys Thr Gly Leu Asn Phe Gly  
180 185 190

Lys Val Asp Val Gly Arg Tyr Thr Asp Val Ser Thr Arg Tyr Lys Val  
195 200 205

Ser Thr Ser Pro Leu Thr Lys Gln Leu Pro Thr Leu Ile Leu Phe Gln  
210 215 220

Gly Gly Lys Glu Ala Met Arg Arg Pro Gln Ile Asp Lys Lys Gly Arg  
225 230 235 240

Ala Val Ser Trp Thr Phe Ser Glu Glu Asn Val Ile Arg Glu Phe Asn  
245 250 255

Leu Asn Glu Leu Tyr Gln Arg Ala Lys Lys Leu Ser Lys Ala Gly Asp  
260 265 270

Asn Ile Pro Glu Glu Gln Pro Val Ala Ser Thr Pro Thr Thr Val Ser  
275 280 285

Asp Gly Glu Asn Lys Lys Asp Lys  
290 295

<210> 208

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 208

gcttgatatt tcgcatgggc ctac

<210> 209  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 209  
 tggagacaat atccctgagg 20

<210> 210  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 210  
 aacagttggc cacagcatgg cagg 24

<210> 211  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 211  
 ccattgatga ggaactagaa cgggacaaga gggtcacttg gattgtggag 50

<210> 212  
 <211> 1985  
 <212> DNA  
 <213> Homo sapiens

<400> 212  
 ggacagctcg cggcccccca gagctctagc cgtcgaggag ctgcctgggg acgtttgccc 60  
 tggggcccca gcctggcccg ggtcaccctg gcatgaggag atgggcctgt tgctcctggt 120  
 cccattgctc ctgctgcccc gctcctacgg actgcccttc tacaacggct tctactactc 180  
 caacagcgcc aacgaccaga acctaggcaa cggtcatggc aaagacctcc ttaatggagt 240  
 gaagctgggtg gtggagacac ccgaggagac cctgttcacc taccaagggg ccagtgtgat 300  
 cctgccctgc cgctaccgct acgagccggc cctgggtctcc ccgcggcgtg tgcgtgtcaa 360  
 atggtggaag ctgtcggaga acggggcccc agagaaggac gtgctggtgg ccatcgggct 420  
 gaggcaccgc tcctttgggg actaccaagg ccgcgtgcac ctgcggcagg acaaagagca 480  
 tgacgtctcg ctggagatcc aggatctgcg gctggaggac tatgggcgtt accgctgtga 540  
 ggtcattgac gggctggagg atgaaagcgg tctggtggag ctggagctgc ggggtgtggt 600

```
<210> 213
<211> 360
<212> PRT
<213> Homo sapiens
```

```

<400> 213
Met Gly Leu Leu Leu Leu Val Pro Leu Leu Leu Leu Pro Gly Ser Tyr
  1             5             10             15

Gly Leu Pro Phe Tyr Asn Gly Phe Tyr Tyr Ser Asn Ser Ala Asn Asp
  20             25             30

Gln Asn Leu Gly Asn Gly His Gly Lys Asp Leu Leu Asn Gly Val Lys
  35             40             45

Leu Val Val Glu Thr Pro Glu Glu Thr Leu Phe Thr Tyr Gln Gly Ala
  50             55             60

Ser Val Ile Leu Pro Cys Arg Tyr Arg Tyr Glu Pro Ala Leu Val Ser
  65             70             75             80

Pro Arg Arg Val Arg Val Lys Trp Trp Lys Leu Ser Glu Asn Gly Ala
  85             90             95

Pro Glu Lys Asp Val Leu Val Ala Ile Gly Leu Arg His Arg Ser Phe
 100             105             110

Gly Asp Tyr Gln Gly Arg Val His Leu Arg Gln Asp Lys Glu His Asp

```

| 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Ser | Leu | Glu | Ile | Gln | Asp | Leu | Arg | Leu | Glu | Asp | Tyr | Gly | Arg | Tyr |  |
| 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |  |
| Arg | Cys | Glu | Val | Ile | Asp | Gly | Leu | Glu | Asp | Glu | Ser | Gly | Leu | Val | Glu |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Leu | Glu | Leu | Arg | Gly | Val | Val | Phe | Pro | Tyr | Gln | Ser | Pro | Asn | Gly | Arg |  |
|     |     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |  |
| Tyr | Gln | Phe | Asn | Phe | His | Glu | Gly | Gln | Gln | Val | Cys | Ala | Glu | Gln | Ala |  |
|     |     |     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |  |
| Ala | Val | Val | Ala | Ser | Phe | Glu | Gln | Leu | Phe | Arg | Ala | Trp | Glu | Glu | Gly |  |
| 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |     |  |
| Leu | Asp | Trp | Cys | Asn | Ala | Gly | Trp | Leu | Gln | Asp | Ala | Thr | Val | Gln | Tyr |  |
| 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |  |
| Pro | Ile | Met | Leu | Pro | Arg | Gln | Pro | Cys | Gly | Gly | Pro | Gly | Leu | Ala | Pro |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |
| Gly | Val | Arg | Ser | Tyr | Gly | Pro | Arg | His | Arg | Arg | Leu | His | Arg | Tyr | Asp |  |
|     |     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |  |
| Val | Phe | Cys | Phe | Ala | Thr | Ala | Leu | Lys | Gly | Arg | Val | Tyr | Tyr | Leu | Glu |  |
|     |     |     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |  |
| His | Pro | Glu | Lys | Leu | Thr | Leu | Thr | Glu | Ala | Arg | Glu | Ala | Cys | Gln | Glu |  |
| 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     |     |  |
| Asp | Asp | Ala | Thr | Ile | Ala | Lys | Val | Gly | Gln | Leu | Phe | Ala | Ala | Trp | Lys |  |
| 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |     |  |
| Phe | His | Gly | Leu | Asp | Arg | Cys | Asp | Ala | Gly | Trp | Leu | Ala | Asp | Gly | Ser |  |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |  |
| Val | Arg | Tyr | Pro | Val | Val | His | Pro | His | Pro | Asn | Cys | Gly | Pro | Pro | Glu |  |
|     |     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |  |
| Pro | Gly | Val | Arg | Ser | Phe | Gly | Phe | Pro | Asp | Pro | Gln | Ser | Arg | Leu | Tyr |  |
| 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |     |     |     |  |
| Gly | Val | Tyr | Cys | Tyr | Arg | Gln | His |     |     |     |     |     |     |     |     |  |
| 355 |     |     |     |     | 360 |     |     |     |     |     |     |     |     |     |     |  |

&lt;210&gt; 214

&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 214  
tgcttcgcta ctgccctc 18

<210> 215  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 215  
ttcccttggtg gggtggag 18

<210> 216  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 216  
agggtggaa gccagttc 18

<210> 217  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 217  
agccagtgcg gaaatgcg 18

<210> 218  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 218  
tgtccaaagt acacacacct gagg 24

<210> 219  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 219  
 gatgccacga tcgccaaggt gggacagctc tttgccgcct ggaag 45

<210> 220  
 <211> 1503  
 <212> DNA  
 <213> Homo sapiens

<400> 220  
 ggagagcgga gcgaagctgg ataacagggg accgatgatg tggcgaccaa cagttctgct 60  
 gcttctgttg ctactgaggc acggggccca ggggaagcca tccccagacg caggccctca 120  
 tggccagggg aggggtgcacc aggcggcccc cctgagcgac gctccccatg atgacgcca 180  
 cgggaacttc cagtacgacc atgaggcttt cctgggacgg gaagtggcca aggaattcga 240  
 ccaactcacc ccagaggaaa gccaggcccc tctggggcgg atcgtggacc gcatggaccg 300  
 cgcgggggac ggcgacggct ggggtgtcgt ggccgagctt cgcgcgtgga tcgcgcacac 360  
 gcagcagcgg cacatacggg actcggtag cgcggcctgg gacacgtacg acacggaccg 420  
 cgacgggcgt gtgggttggg aggagctgcg caacgccacc tatggccact acgcgcccgg 480  
 tgaagaattt catgacgtgg aggatgcaga gacctacaaa aagatgctgg ctcgggacga 540  
 gcggcgtttc cgggtggccg accaggatgg ggactcgatg gccactcgag aggagctgac 600  
 agccttcctg caccocgagg agttccctca catgcgggac atcgtgattg ctgaaaccct 660  
 ggaggacctg gacagaaaca aagatggcta tgtccagggtg gaggagtaca tcgcggatct 720  
 gtactcagcc gagcctgggg aggaggagcc ggcgtgggtg cagacggaga ggcagcagtt 780  
 ccgggacttc cgggatctga acaaggatgg gcacctggat gggagtgagg tgggccactg 840  
 ggtgctgccc cctgcccagg accagcccct ggtggaagcc aaccacctgc tgcacgagag 900  
 cgacacggac aaggatgggc ggctgagcaa agcggaaatc ctgggtaatt ggaacatgtt 960  
 tgtgggcagt caggccacca actatggcga ggacctgacc cggcaccacg atgagctgtg 1020  
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 tgggtctggc ccctccctgt ccaggccccg caggaggcag atgcagtccc aggcatcctc 1140  
 ctgcccctgg gctctcaggg accccctggg tcggcttctg tcctgtcac accccaacc 1200  
 ccagggaggg gctgtcatag tcccagagga taagcaatac ctatttctga ctgagtctcc 1260  
 cagcccagac ccagggaccc ttggccccc aaactgactc aagaaccgcc ccaaccctc 1320  
 cagctccaaa tctgagcctc caccacatag actgaaactc ccctggcccc agcctctctc 1380  
 tgccctggcct ggcctgggac acctcctctc tgccaggagg caataaaagc cagcgccggg 1440  
 accttgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500  
 aaa 1503

<210> 221  
 <211> 328  
 <212> PRT  
 <213> Homo sapiens

<400> 221  
 Met Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Arg His

|   |     |     |     |
|---|-----|-----|-----|
| 1   | 5   | 10  | 15  |
| Gly Ala Gln Gly Lys Pro Ser Pro Asp Ala Gly Pro His Gly Gln Gly | 20  | 25  | 30  |
| Arg Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Asp Ala | 35  | 40  | 45  |
| His Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val | 50  | 55  | 60  |
| Ala Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu | 65  | 70  | 75  |
| Gly Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp | 85  | 90  | 95  |
| Val Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg | 100 | 105 | 110 |
| His Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp | 115 | 120 | 125 |
| Arg Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Ala Thr Tyr Gly | 130 | 135 | 140 |
| His Tyr Ala Pro Gly Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr | 145 | 150 | 155 |
| Tyr Lys Lys Met Leu Ala Arg Asp Glu Arg Arg Phe Arg Val Ala Asp | 165 | 170 | 175 |
| Gln Asp Gly Asp Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu | 180 | 185 | 190 |
| His Pro Glu Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr | 195 | 200 | 205 |
| Leu Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu | 210 | 215 | 220 |
| Tyr Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Glu Pro Ala | 225 | 230 | 235 |
| Trp Val Gln Thr Glu Arg Gln Gln Phe Arg Asp Phe Arg Asp Leu Asn | 245 | 250 | 255 |
| Lys Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val Leu Pro | 260 | 265 | 270 |
| Pro Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu Leu His Glu | 275 | 280 | 285 |

09905056 04001

Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Glu Ile Leu Gly  
 290 295 300

Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp  
 305 310 315 320

Leu Thr Arg His His Asp Glu Leu  
 325

<210> 222

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 222

cgcaggccct catggccagg

20

<210> 223

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 223

gaaatcctgg gtaattgg

18

<210> 224

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 224

gtgcgcggtg ctcacagctc atc

23

<210> 225

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe



<400> 225  
 cccccctgag cgacgcctccc ccatgatgac gcccacggga actt

44

<210> 226  
 <211> 2403  
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<213> Homo sapiens

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<400> 245

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| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |
| Ala | Thr | Ala | Thr | Val | Pro | Val | Val | Pro | Trp | His | Val | Pro | Cys |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |
| Pro | Gln | Cys | Ala | Cys | Gln | Ile | Arg | Pro | Trp | Tyr | Thr | Pro | Arg |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |
| Ser | Tyr | Arg | Glu | Ala | Thr | Thr | Val | Asp | Cys | Asn | Asp | Leu | Phe |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |
| Thr | Ala | Val | Pro | Pro | Ala | Leu | Pro | Ala | Gly | Thr | Gln | Thr | Leu |
|     |     |     |     | 65  |     |     |     | 70  |     |     |     |     | 75  |
| Leu | Gln | Ser | Asn | Ser | Ile | Val | Arg | Val | Asp | Gln | Ser | Glu | Leu |
|     |     |     |     | 80  |     |     |     | 85  |     |     |     |     | 90  |
| Tyr | Leu | Ala | Asn | Leu | Thr | Glu | Leu | Asp | Leu | Ser | Gln | Asn | Ser |
|     |     |     |     | 95  |     |     |     | 100 |     |     |     |     | 105 |
| Ser | Asp | Ala | Arg | Asp | Cys | Asp | Phe | His | Ala | Leu | Pro | Gln | Leu |
|     |     |     |     | 110 |     |     |     | 115 |     |     |     |     | 120 |
| Ser | Leu | His | Leu | Glu | Glu | Asn | Gln | Leu | Thr | Arg | Leu | Glu | Asp |
|     |     |     |     | 125 |     |     |     | 130 |     |     |     |     | 135 |
| Ser | Phe | Ala | Gly | Leu | Ala | Ser | Leu | Gln | Glu | Leu | Tyr | Leu | Asn |
|     |     |     |     | 140 |     |     |     | 145 |     |     |     |     | 150 |

|                     |                     |                         |
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| 155                 | 160                 | 165                     |
| Asn Leu Leu Arg     | Leu His Leu Asn Ser | Asn Leu Leu Arg Ala Ile |
| 170                 | 175                 | 180                     |
| Asp Ser Arg Trp     | Phe Glu Met Leu Pro | Asn Leu Glu Ile Leu Met |
| 185                 | 190                 | 195                     |
| Ile Gly Gly Asn     | Lys Val Asp Ala Ile | Leu Asp Met Asn Phe Arg |
| 200                 | 205                 | 210                     |
| Pro Leu Ala Asn     | Leu Arg Ser Leu Val | Leu Ala Gly Met Asn Leu |
| 215                 | 220                 | 225                     |
| Arg Glu Ile Ser     | Asp Tyr Ala Leu Glu | Gly Leu Gln Ser Leu Glu |
| 230                 | 235                 | 240                     |
| Ser Leu Ser Phe     | Tyr Asp Asn Gln Leu | Ala Arg Val Pro Arg Arg |
| 245                 | 250                 | 255                     |
| Ala Leu Glu Gln     | Val Pro Gly Leu Lys | Phe Leu Asp Leu Asn Lys |
| 260                 | 265                 | 270                     |
| Asn Pro Leu Gln     | Arg Val Gly Pro Gly | Asp Phe Ala Asn Met Leu |
| 275                 | 280                 | 285                     |
| His Leu Lys Glu     | Leu Gly Leu Asn Asn | Met Glu Glu Leu Val Ser |
| 290                 | 295                 | 300                     |
| Ile Asp Lys Phe     | Ala Leu Val Asn Leu | Pro Glu Leu Thr Lys Leu |
| 305                 | 310                 | 315                     |
| Asp Ile Thr Asn     | Asn Pro Arg Leu Ser | Phe Ile His Pro Arg Ala |
| 320                 | 325                 | 330                     |
| Phe His His Leu     | Pro Gln Met Glu Thr | Leu Met Leu Asn Asn Asn |
| 335                 | 340                 | 345                     |
| Ala Leu Ser Ala     | Leu His Gln Gln Thr | Val Glu Ser Leu Pro Asn |
| 350                 | 355                 | 360                     |
| Leu Gln Glu Val     | Gly Leu His Gly Asn | Pro Ile Arg Cys Asp Cys |
| 365                 | 370                 | 375                     |
| Val Ile Arg Trp     | Ala Asn Ala Thr Gly | Thr Arg Val Arg Phe Ile |
| 380                 | 385                 | 390                     |
| Glu Pro Gln Ser     | Thr Leu Cys Ala Glu | Pro Pro Asp Leu Gln Arg |
| 395                 | 400                 | 405                     |
| Leu Pro Val Arg     | Glu Val Pro Phe Arg | Glu Met Thr Asp His Cys |

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| Leu Pro Leu Ile Ser Pro Arg Ser Phe Pro Pro Ser Leu Gln Val | 425 |  | 430 |  | 435 |
| Ala Ser Gly Glu Ser Met Val Leu His Cys Arg Ala Leu Ala Glu | 440 |  | 445 |  | 450 |
| Pro Glu Pro Glu Ile Tyr Trp Val Thr Pro Ala Gly Leu Arg Leu | 455 |  | 460 |  | 465 |
| Thr Pro Ala His Ala Gly Arg Arg Tyr Arg Val Tyr Pro Glu Gly | 470 |  | 475 |  | 480 |
| Thr Leu Glu Leu Arg Arg Val Thr Ala Glu Glu Ala Gly Leu Tyr | 485 |  | 490 |  | 495 |
| Thr Cys Val Ala Gln Asn Leu Val Gly Ala Asp Thr Lys Thr Val | 500 |  | 505 |  | 510 |
| Ser Val Val Val Gly Arg Ala Leu Leu Gln Pro Gly Arg Asp Glu | 515 |  | 520 |  | 525 |
| Gly Gln Gly Leu Glu Leu Arg Val Gln Glu Thr His Pro Tyr His | 530 |  | 535 |  | 540 |
| Ile Leu Leu Ser Trp Val Thr Pro Pro Asn Thr Val Ser Thr Asn | 545 |  | 550 |  | 555 |
| Leu Thr Trp Ser Ser Ala Ser Ser Leu Arg Gly Gln Gly Ala Thr | 560 |  | 565 |  | 570 |
| Ala Leu Ala Arg Leu Pro Arg Gly Thr His Ser Tyr Asn Ile Thr | 575 |  | 580 |  | 585 |
| Arg Leu Leu Gln Ala Thr Glu Tyr Trp Ala Cys Leu Gln Val Ala | 590 |  | 595 |  | 600 |
| Phe Ala Asp Ala His Thr Gln Leu Ala Cys Val Trp Ala Arg Thr | 605 |  | 610 |  | 615 |
| Lys Glu Ala Thr Ser Cys His Arg Ala Leu Gly Asp Arg Pro Gly | 620 |  | 625 |  | 630 |
| Leu Ile Ala Ile Leu Ala Leu Ala Val Leu Leu Leu Ala Ala Gly | 635 |  | 640 |  | 645 |
| Leu Ala Ala His Leu Gly Thr Gly Gln Pro Arg Lys Gly Val Gly | 650 |  | 655 |  | 660 |
| Gly Arg Arg Pro Leu Pro Pro Ala Trp Ala Phe Trp Gly Trp Ser | 665 |  | 670 |  | 675 |

Ala Pro Ser Val Arg Val Val Ser Ala Pro Leu Val Leu Pro Trp  
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Asn Pro Gly Arg Lys Leu Pro Arg Ser Ser Glu Gly Glu Thr Leu  
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Leu Pro Pro Leu Ser Gln Asn Ser  
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<212> PRT

<213> Homo Sapien

<400> 250

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| Met | Arg | Gln | Thr | Ile | Ile | Lys | Val | Ile | Lys | Phe | Ile | Leu | Ile | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Tyr | Thr | Val | Tyr | Tyr | Val | His | Asn | Ile | Lys | Phe | Asp | Val | Asp |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Thr | Val | Asp | Ile | Glu | Ser | Leu | Thr | Gly | Tyr | Arg | Thr | Tyr | Arg |
|     |     |     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Ala | His | Pro | Leu | Ala | Thr | Leu | Phe | Lys | Ile | Leu | Ala | Ser | Phe |
|     |     |     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Ile | Ser | Leu | Val | Ile | Phe | Tyr | Gly | Leu | Ile | Cys | Met | Tyr | Thr |
|     |     |     |     | 65  |     |     |     |     | 70  |     |     |     | 75  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Trp | Trp | Met | Leu | Arg | Arg | Ser | Leu | Lys | Lys | Tyr | Ser | Phe | Glu |
|     |     |     |     | 80  |     |     |     |     | 85  |     |     |     | 90  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ile | Arg | Glu | Glu | Ser | Ser | Tyr | Ser | Asp | Ile | Pro | Asp | Val | Lys |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

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|-----------------|---------------------|---------------------|-----|--|-----|
|                 | 95                  |                     | 100 |  | 105 |
| Asn Asp Phe Ala | Phe Met Leu His Leu | Ile Asp Gln Tyr Asp | Pro |  |     |
|                 | 110                 | 115                 | 120 |  |     |
| Leu Tyr Ser Lys | Arg Phe Ala Val Phe | Leu Ser Glu Val Ser | Glu |  |     |
|                 | 125                 | 130                 | 135 |  |     |
| Asn Lys Leu Arg | Gln Leu Asn Leu Asn | Asn Glu Trp Thr Leu | Asp |  |     |
|                 | 140                 | 145                 | 150 |  |     |
| Lys Leu Arg Gln | Arg Leu Thr Lys Asn | Ala Gln Asp Lys Leu | Glu |  |     |
|                 | 155                 | 160                 | 165 |  |     |
| Leu His Leu Phe | Met Leu Ser Gly Ile | Pro Asp Thr Val Phe | Asp |  |     |
|                 | 170                 | 175                 | 180 |  |     |
| Leu Val Glu Leu | Glu Val Leu Lys Leu | Glu Leu Ile Pro Asp | Val |  |     |
|                 | 185                 | 190                 | 195 |  |     |
| Thr Ile Pro Pro | Ser Ile Ala Gln Leu | Thr Gly Leu Lys Glu | Leu |  |     |
|                 | 200                 | 205                 | 210 |  |     |
| Trp Leu Tyr His | Thr Ala Ala Lys Ile | Glu Ala Pro Ala Leu | Ala |  |     |
|                 | 215                 | 220                 | 225 |  |     |
| Phe Leu Arg Glu | Asn Leu Arg Ala Leu | His Ile Lys Phe Thr | Asp |  |     |
|                 | 230                 | 235                 | 240 |  |     |
| Ile Lys Glu Ile | Pro Leu Trp Ile Tyr | Ser Leu Lys Thr Leu | Glu |  |     |
|                 | 245                 | 250                 | 255 |  |     |
| Glu Leu His Leu | Thr Gly Asn Leu Ser | Ala Glu Asn Asn Arg | Tyr |  |     |
|                 | 260                 | 265                 | 270 |  |     |
| Ile Val Ile Asp | Gly Leu Arg Glu Leu | Lys Arg Leu Lys Val | Leu |  |     |
|                 | 275                 | 280                 | 285 |  |     |
| Arg Leu Lys Ser | Asn Leu Ser Lys Leu | Pro Gln Val Val Thr | Asp |  |     |
|                 | 290                 | 295                 | 300 |  |     |
| Val Gly Val His | Leu Gln Lys Leu Ser | Ile Asn Asn Glu Gly | Thr |  |     |
|                 | 305                 | 310                 | 315 |  |     |
| Lys Leu Ile Val | Leu Asn Ser Leu Lys | Lys Met Ala Asn Leu | Thr |  |     |
|                 | 320                 | 325                 | 330 |  |     |
| Glu Leu Glu Leu | Ile Arg Cys Asp Leu | Glu Arg Ile Pro His | Ser |  |     |
|                 | 335                 | 340                 | 345 |  |     |
| Ile Phe Ser Leu | His Asn Leu Gln Glu | Ile Asp Leu Lys Asp | Asn |  |     |
|                 | 350                 | 355                 | 360 |  |     |

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Leu | Lys | Thr | Ile | Glu | Glu | Ile | Ile | Ser | Phe | Gln | His | Leu | His |
|     |     |     |     | 365 |     |     |     |     | 370 |     |     |     |     | 375 |
| Arg | Leu | Thr | Cys | Leu | Lys | Leu | Trp | Tyr | Asn | His | Ile | Ala | Tyr | Ile |
|     |     |     |     | 380 |     |     |     |     | 385 |     |     |     |     | 390 |
| Pro | Ile | Gln | Ile | Gly | Asn | Leu | Thr | Asn | Leu | Glu | Arg | Leu | Tyr | Leu |
|     |     |     |     | 395 |     |     |     |     | 400 |     |     |     |     | 405 |
| Asn | Arg | Asn | Lys | Ile | Glu | Lys | Ile | Pro | Thr | Gln | Leu | Phe | Tyr | Cys |
|     |     |     |     | 410 |     |     |     |     | 415 |     |     |     |     | 420 |
| Arg | Lys | Leu | Arg | Tyr | Leu | Asp | Leu | Ser | His | Asn | Asn | Leu | Thr | Phe |
|     |     |     |     | 425 |     |     |     |     | 430 |     |     |     |     | 435 |
| Leu | Pro | Ala | Asp | Ile | Gly | Leu | Leu | Gln | Asn | Leu | Gln | Asn | Leu | Ala |
|     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |     | 450 |
| Ile | Thr | Ala | Asn | Arg | Ile | Glu | Thr | Leu | Pro | Pro | Glu | Leu | Phe | Gln |
|     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     | 465 |
| Cys | Arg | Lys | Leu | Arg | Ala | Leu | His | Leu | Gly | Asn | Asn | Val | Leu | Gln |
|     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |
| Ser | Leu | Pro | Ser | Arg | Val | Gly | Glu | Leu | Thr | Asn | Leu | Thr | Gln | Ile |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |
| Glu | Leu | Arg | Gly | Asn | Arg | Leu | Glu | Cys | Leu | Pro | Val | Glu | Leu | Gly |
|     |     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |
| Glu | Cys | Pro | Leu | Leu | Lys | Arg | Ser | Gly | Leu | Val | Val | Glu | Glu | Asp |
|     |     |     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |
| Leu | Phe | Asn | Thr | Leu | Pro | Pro | Glu | Val | Lys | Glu | Arg | Leu | Trp | Arg |
|     |     |     |     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |
| Ala | Asp | Lys | Glu | Gln | Ala |     |     |     |     |     |     |     |     |     |
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&lt;211&gt; 20

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&lt;210&gt; 252

&lt;211&gt; 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 252

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<210> 253

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 253

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<210> 254

<211> 1650

<212> DNA

<213> Homo Sapien

<400> 254

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<211> 452

<212> PRT

<213> Homo Sapien

<400> 255

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Leu | Ala | Leu | Arg | Arg | Ser | Pro | Val | Pro | Arg | Trp | Leu | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Leu | Pro | Leu | Leu | Leu | Gly | Leu | Asn | Ala | Gly | Ala | Val | Ile | Asp |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Pro | Thr | Glu | Glu | Gly | Lys | Glu | Val | Trp | Asp | Tyr | Val | Thr | Val |
|     |     |     | 35  |     |     |     |     |     | 40  |     |     |     | 45  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Arg | Lys | Asp | Ala | Tyr | Met | Phe | Trp | Trp | Leu | Tyr | Tyr | Ala | Thr | Asn |  |
|     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |  |
| Ser | Cys | Lys | Asn | Phe | Ser | Glu | Leu | Pro | Leu | Val | Met | Trp | Leu | Gln |  |
|     |     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |  |
| Gly | Gly | Pro | Gly | Gly | Ser | Ser | Thr | Gly | Phe | Gly | Asn | Phe | Glu | Glu |  |
|     |     |     |     | 80  |     |     |     |     | 85  |     |     |     |     | 90  |  |
| Ile | Gly | Pro | Leu | Asp | Ser | Asp | Leu | Lys | Pro | Arg | Lys | Thr | Thr | Trp |  |
|     |     |     |     | 95  |     |     |     |     | 100 |     |     |     |     | 105 |  |
| Leu | Gln | Ala | Ala | Ser | Leu | Leu | Phe | Val | Asp | Asn | Pro | Val | Gly | Thr |  |
|     |     |     |     | 110 |     |     |     |     | 115 |     |     |     |     | 120 |  |
| Gly | Phe | Ser | Tyr | Val | Asn | Gly | Ser | Gly | Ala | Tyr | Ala | Lys | Asp | Leu |  |
|     |     |     |     | 125 |     |     |     |     | 130 |     |     |     |     | 135 |  |
| Ala | Met | Val | Ala | Ser | Asp | Met | Met | Val | Leu | Leu | Lys | Thr | Phe | Phe |  |
|     |     |     |     | 140 |     |     |     |     | 145 |     |     |     |     | 150 |  |
| Ser | Cys | His | Lys | Glu | Phe | Gln | Thr | Val | Pro | Phe | Tyr | Ile | Phe | Ser |  |
|     |     |     |     | 155 |     |     |     |     | 160 |     |     |     |     | 165 |  |
| Glu | Ser | Tyr | Gly | Gly | Lys | Met | Ala | Ala | Gly | Ile | Gly | Leu | Glu | Leu |  |
|     |     |     |     | 170 |     |     |     |     | 175 |     |     |     |     | 180 |  |
| Tyr | Lys | Ala | Ile | Gln | Arg | Gly | Thr | Ile | Lys | Cys | Asn | Phe | Ala | Gly |  |
|     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |     | 195 |  |
| Val | Ala | Leu | Gly | Asp | Ser | Trp | Ile | Ser | Pro | Val | Asp | Ser | Val | Leu |  |
|     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     | 210 |  |
| Ser | Trp | Gly | Pro | Tyr | Leu | Tyr | Ser | Met | Ser | Leu | Leu | Glu | Asp | Lys |  |
|     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     | 225 |  |
| Gly | Leu | Ala | Glu | Val | Ser | Lys | Val | Ala | Glu | Gln | Val | Leu | Asn | Ala |  |
|     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |
| Val | Asn | Lys | Gly | Leu | Tyr | Arg | Glu | Ala | Thr | Glu | Leu | Trp | Gly | Lys |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |  |
| Ala | Glu | Met | Ile | Ile | Glu | Gln | Asn | Thr | Asp | Gly | Val | Asn | Phe | Tyr |  |
|     |     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |  |
| Asn | Ile | Leu | Thr | Lys | Ser | Thr | Pro | Thr | Ser | Thr | Met | Glu | Ser | Ser |  |
|     |     |     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |  |
| Leu | Glu | Phe | Thr | Gln | Ser | His | Leu | Val | Cys | Leu | Cys | Gln | Arg | His |  |
|     |     |     |     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |  |
| Val | Arg | His | Leu | Gln | Arg | Asp | Ala | Leu | Ser | Gln | Leu | Met | Asn | Gly |  |

|                 |                     |                         |     |     |     |
|-----------------|---------------------|-------------------------|-----|-----|-----|
|                 | 305                 |                         | 310 |     | 315 |
| Pro Ile Arg Lys | Lys Leu Lys Ile Ile | Pro Glu Asp Gln Ser Trp |     |     |     |
|                 | 320                 | 325                     |     | 330 |     |
| Gly Gly Gln Ala | Thr Asn Val Phe Val | Asn Met Glu Glu Asp Phe |     |     |     |
|                 | 335                 | 340                     |     | 345 |     |
| Met Lys Pro Val | Ile Ser Ile Val Asp | Glu Leu Leu Glu Ala Gly |     |     |     |
|                 | 350                 | 355                     |     | 360 |     |
| Ile Asn Val Thr | Val Tyr Asn Gly Gln | Leu Asp Leu Ile Val Asp |     |     |     |
|                 | 365                 | 370                     |     | 375 |     |
| Thr Met Gly Gln | Glu Ala Trp Val Arg | Lys Leu Lys Trp Pro Glu |     |     |     |
|                 | 380                 | 385                     |     | 390 |     |
| Leu Pro Lys Phe | Ser Gln Leu Lys Trp | Lys Ala Leu Tyr Ser Asp |     |     |     |
|                 | 395                 | 400                     |     | 405 |     |
| Pro Lys Ser Leu | Glu Thr Ser Ala Phe | Val Lys Ser Tyr Lys Asn |     |     |     |
|                 | 410                 | 415                     |     | 420 |     |
| Leu Ala Phe Tyr | Trp Ile Leu Lys Ala | Gly His Met Val Pro Ser |     |     |     |
|                 | 425                 | 430                     |     | 435 |     |
| Asp Gln Gly Asp | Met Ala Leu Lys Met | Met Arg Leu Val Thr Gln |     |     |     |
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Gln Glu

<210> 256

<211> 1100

<212> DNA

<213> Homo Sapien

<400> 256

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Ser Asp Pro Ser Gly Trp Met Val Gln Phe Gly Gln Leu Thr Ser  
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 Tyr Asp Ile Ala Leu Val Lys Leu Ser Ala Pro Val Thr Tyr Thr  
 140 145 150  
 Lys His Ile Gln Pro Ile Cys Leu Gln Ala Ser Thr Phe Glu Phe  
 155 160 165  
 Glu Asn Arg Thr Asp Cys Trp Val Thr Gly Trp Gly Tyr Ile Lys  
 170 175 180  
 Glu Asp Glu Ala Leu Pro Ser Pro His Thr Leu Gln Glu Val Gln  
 185 190 195  
 Val Ala Ile Ile Asn Asn Ser Met Cys Asn His Leu Phe Leu Lys  
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 Tyr Ser Phe Arg Lys Asp Ile Phe Gly Asp Met Val Cys Ala Gly  
 215 220 225  
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 230 235 240  
 Pro Leu Ala Cys Asn Lys Asn Gly Leu Trp Tyr Gln Ile Gly Val  
 245 250 255  
 Val Ser Trp Gly Val Gly Cys Gly Arg Pro Asn Arg Pro Gly Val  
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 Tyr Thr Asn Ile Ser His His Phe Glu Trp Ile Gln Lys Leu Met  
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<213> Homo Sapien

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<211> 556

<212> PRT

<213> Homo Sapien

<400> 259

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| Met | Gly | Leu | Gln | Ala | Cys | Leu | Leu | Gly | Leu | Phe | Ala | Leu | Ile | Leu |
| 1   |     |     |     |     | 5   |     |     | 10  |     |     |     |     | 15  |     |

Ser Gly Lys Cys Ser Tyr Ser Pro Glu Pro Asp Gln Arg Arg Thr



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Asn | Ile | Ser | Thr | Trp | Val | Tyr | Ser | Ser | Pro | Gly | Arg | His | Glu | Gly |  |
|     |     |     |     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |  |
| Gln | Glu | Pro | Phe | Leu | Gln | Trp | Leu | Met | Leu | Leu | Ser | Asn | Glu | Ser |  |
|     |     |     |     | 305 |     |     |     |     | 310 |     |     |     |     | 315 |  |
| Ala | Leu | Pro | His | Val | His | Thr | Val | Ser | Tyr | Gly | Asp | Asp | Glu | Asp |  |
|     |     |     |     | 320 |     |     |     |     | 325 |     |     |     |     | 330 |  |
| Ser | Leu | Ser | Ser | Ala | Tyr | Ile | Gln | Arg | Val | Asn | Thr | Glu | Leu | Met |  |
|     |     |     |     | 335 |     |     |     |     | 340 |     |     |     |     | 345 |  |
| Lys | Ala | Ala | Ala | Arg | Gly | Leu | Thr | Leu | Leu | Phe | Ala | Ser | Gly | Asp |  |
|     |     |     |     | 350 |     |     |     |     | 355 |     |     |     |     | 360 |  |
| Ser | Gly | Ala | Gly | Cys | Trp | Ser | Val | Ser | Gly | Arg | His | Gln | Phe | Arg |  |
|     |     |     |     | 365 |     |     |     |     | 370 |     |     |     |     | 375 |  |
| Pro | Thr | Phe | Pro | Ala | Ser | Ser | Pro | Tyr | Val | Thr | Thr | Val | Gly | Gly |  |
|     |     |     |     | 380 |     |     |     |     | 385 |     |     |     |     | 390 |  |
| Thr | Ser | Phe | Gln | Glu | Pro | Phe | Leu | Ile | Thr | Asn | Glu | Ile | Val | Asp |  |
|     |     |     |     | 395 |     |     |     |     | 400 |     |     |     |     | 405 |  |
| Tyr | Ile | Ser | Gly | Gly | Gly | Phe | Ser | Asn | Val | Phe | Pro | Arg | Pro | Ser |  |
|     |     |     |     | 410 |     |     |     |     | 415 |     |     |     |     | 420 |  |
| Tyr | Gln | Glu | Glu | Ala | Val | Thr | Lys | Phe | Leu | Ser | Ser | Ser | Pro | His |  |
|     |     |     |     | 425 |     |     |     |     | 430 |     |     |     |     | 435 |  |
| Leu | Pro | Pro | Ser | Ser | Tyr | Phe | Asn | Ala | Ser | Gly | Arg | Ala | Tyr | Pro |  |
|     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |     | 450 |  |
| Asp | Val | Ala | Ala | Leu | Ser | Asp | Gly | Tyr | Trp | Val | Val | Ser | Asn | Arg |  |
|     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     | 465 |  |
| Val | Pro | Ile | Pro | Trp | Val | Ser | Gly | Thr | Ser | Ala | Ser | Thr | Pro | Val |  |
|     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |  |
| Phe | Gly | Gly | Ile | Leu | Ser | Leu | Ile | Asn | Glu | His | Arg | Ile | Leu | Ser |  |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |  |
| Gly | Arg | Pro | Pro | Leu | Gly | Phe | Leu | Asn | Pro | Arg | Leu | Tyr | Gln | Gln |  |
|     |     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |  |
| His | Gly | Ala | Gly | Leu | Phe | Asp | Val | Thr | Arg | Gly | Cys | His | Glu | Ser |  |
|     |     |     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |  |
| Cys | Leu | Asp | Glu | Glu | Val | Glu | Gly | Gln | Gly | Phe | Cys | Ser | Gly | Pro |  |
|     |     |     |     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |  |
| Gly | Trp | Asp | Pro | Val | Thr | Gly | Trp | Gly | Thr | Pro | Thr | Ser | Gln | Leu |  |
|     |     |     |     | 545 |     |     |     |     | 550 |     |     |     |     | 555 |  |

Cys

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&lt;211&gt; 1638

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 260

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<212> PRT
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| Met | Ala | Gly | Ile | Pro | Gly | Leu | Leu | Phe | Leu | Leu | Phe | Phe | Leu | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |
| Cys | Ala | Val | Gly | Gln | Val | Ser | Pro | Tyr | Ser | Ala | Pro | Trp | Lys | Pro |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |
| Thr | Trp | Pro | Ala | Tyr | Arg | Leu | Pro | Val | Val | Leu | Pro | Gln | Ser | Thr |
|     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |
| Leu | Asn | Leu | Ala | Lys | Pro | Asp | Phe | Gly | Ala | Glu | Ala | Lys | Leu | Glu |
|     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |
| Val | Ser | Ser | Ser | Cys | Gly | Pro | Gln | Cys | His | Lys | Gly | Thr | Pro | Leu |
|     |     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |
| Pro | Thr | Tyr | Glu | Glu | Ala | Lys | Gln | Tyr | Leu | Ser | Tyr | Glu | Thr | Leu |
|     |     |     |     | 80  |     |     |     |     | 85  |     |     |     |     | 90  |
| Tyr | Ala | Asn | Gly | Ser | Arg | Thr | Glu | Thr | Gln | Val | Gly | Ile | Tyr | Ile |
|     |     |     |     | 95  |     |     |     |     | 100 |     |     |     |     | 105 |
| Leu | Ser | Ser | Ser | Gly | Asp | Gly | Ala | Gln | His | Arg | Asp | Ser | Gly | Ser |
|     |     |     |     | 110 |     |     |     |     | 115 |     |     |     |     | 120 |



|     |     |     |     |  |            |     |     |     |     |            |     |     |     |     |            |
|-----|-----|-----|-----|--|------------|-----|-----|-----|-----|------------|-----|-----|-----|-----|------------|
| Ser | Gly | Lys | Ser |  | Arg<br>125 | Arg | Lys | Arg | Gln | Ile<br>130 | Tyr | Gly | Tyr | Asp | Ser<br>135 |
| Arg | Phe | Ser | Ile |  | Phe<br>140 | Gly | Lys | Asp | Phe | Leu<br>145 | Leu | Asn | Tyr | Pro | Phe<br>150 |
| Ser | Thr | Ser | Val |  | Lys<br>155 | Leu | Ser | Thr | Gly | Cys<br>160 | Thr | Gly | Thr | Leu | Val<br>165 |
| Ala | Glu | Lys | His |  | Val<br>170 | Leu | Thr | Ala | Ala | His<br>175 | Cys | Ile | His | Asp | Gly<br>180 |
| Lys | Thr | Tyr | Val |  | Lys<br>185 | Gly | Thr | Gln | Lys | Leu<br>190 | Arg | Val | Gly | Phe | Leu<br>195 |
| Lys | Pro | Lys | Phe |  | Lys<br>200 | Asp | Gly | Gly | Arg | Gly<br>205 | Ala | Asn | Asp | Ser | Thr<br>210 |
| Ser | Ala | Met | Pro |  | Glu<br>215 | Gln | Met | Lys | Phe | Gln<br>220 | Trp | Ile | Arg | Val | Lys<br>225 |
| Arg | Thr | His | Val |  | Pro<br>230 | Lys | Gly | Trp | Ile | Lys<br>235 | Gly | Asn | Ala | Asn | Asp<br>240 |
| Ile | Gly | Met | Asp |  | Tyr<br>245 | Asp | Tyr | Ala | Leu | Leu<br>250 | Glu | Leu | Lys | Lys | Pro<br>255 |
| His | Lys | Arg | Lys |  | Phe<br>260 | Met | Lys | Ile | Gly | Val<br>265 | Ser | Pro | Pro | Ala | Lys<br>270 |
| Gln | Leu | Pro | Gly |  | Gly<br>275 | Arg | Ile | His | Phe | Ser<br>280 | Gly | Tyr | Asp | Asn | Asp<br>285 |
| Arg | Pro | Gly | Asn |  | Leu<br>290 | Val | Tyr | Arg | Phe | Cys<br>295 | Asp | Val | Lys | Asp | Glu<br>300 |
| Thr | Tyr | Asp | Leu |  | Leu<br>305 | Tyr | Gln | Gln | Cys | Asp<br>310 | Ala | Gln | Pro | Gly | Ala<br>315 |
| Ser | Gly | Ser | Gly |  | Val<br>320 | Tyr | Val | Arg | Met | Trp<br>325 | Lys | Arg | Gln | Gln | Gln<br>330 |
| Lys | Trp | Glu | Arg |  | Lys<br>335 | Ile | Ile | Gly | Ile | Phe<br>340 | Ser | Gly | His | Gln | Trp<br>345 |
| Val | Asp | Met | Asn |  | Gly<br>350 | Ser | Pro | Gln | Asp | Phe<br>355 | Asn | Val | Ala | Val | Arg<br>360 |
| Ile | Thr | Pro | Leu |  | Lys<br>365 | Tyr | Ala | Gln | Ile | Cys<br>370 | Tyr | Trp | Ile | Lys | Gly<br>375 |
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 ggagcgggat gcttgtctgg gcgactccgg gggccccctc atgtgccagg 800  
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 gccgagcgca acaggcccgg ggtctacatc agcctctctg cgcaccgctc 900  
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 aataggctca tctacctata cctctggggg cccggacggc tgctgcggaa 1150

aggaaacccc ctccccgacc cgcccgacgg cctcaggccc ccctccaagg 1200  
catcaggccc cgcccaacgg cctcatgtcc ccgccccac gacttccggc 1250  
cccgcccccg ggccccagcg cttttgtgta tataaatgtt aatgattttt 1300  
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<211> 317

<212> PRT

<213> Homo Sapien

<400> 263

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Val | Val | Ser | Gly | Ala | Pro | Pro | Ala | Leu | Gly | Gly | Gly | Cys | Leu | 1   | 5   | 10  | 15 |
| Gly | Thr | Phe | Thr | Ser | Leu | Leu | Leu | Leu | Ala | Ser | Thr | Ala | Ile | Leu | 20  | 25  | 30  |    |
| Asn | Ala | Ala | Arg | Ile | Pro | Val | Pro | Pro | Ala | Cys | Gly | Lys | Pro | Gln | 35  | 40  | 45  |    |
| Gln | Leu | Asn | Arg | Val | Val | Gly | Gly | Glu | Asp | Ser | Thr | Asp | Ser | Glu | 50  | 55  | 60  |    |
| Trp | Pro | Trp | Ile | Val | Ser | Ile | Gln | Lys | Asn | Gly | Thr | His | His | Cys | 65  | 70  | 75  |    |
| Ala | Gly | Ser | Leu | Leu | Thr | Ser | Arg | Trp | Val | Ile | Thr | Ala | Ala | His | 80  | 85  | 90  |    |
| Cys | Phe | Lys | Asp | Asn | Leu | Asn | Lys | Pro | Tyr | Leu | Phe | Ser | Val | Leu | 95  | 100 | 105 |    |
| Leu | Gly | Ala | Trp | Gln | Leu | Gly | Asn | Pro | Gly | Ser | Arg | Ser | Gln | Lys | 110 | 115 | 120 |    |
| Val | Gly | Val | Ala | Trp | Val | Glu | Pro | His | Pro | Val | Tyr | Ser | Trp | Lys | 125 | 130 | 135 |    |
| Glu | Gly | Ala | Cys | Ala | Asp | Ile | Ala | Leu | Val | Arg | Leu | Glu | Arg | Ser | 140 | 145 | 150 |    |
| Ile | Gln | Phe | Ser | Glu | Arg | Val | Leu | Pro | Ile | Cys | Leu | Pro | Asp | Ala | 155 | 160 | 165 |    |
| Ser | Ile | His | Leu | Pro | Pro | Asn | Thr | His | Cys | Trp | Ile | Ser | Gly | Trp | 170 | 175 | 180 |    |

09905056-074304



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<210> 268  
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<223> Synthetic Oligonucleotide Probe

<400> 268  
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<210> 270  
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<210> 272  
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<220>  
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<400> 272  
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<210> 273  
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<400> 273  
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<210> 274  
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<400> 274  
ggcgaagagc agggtagac cccg 24

<210> 275  
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<212> DNA  
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<210> 277  
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<220>  
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<400> 277  
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<210> 278  
<211> 18  
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<400> 278  
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<210> 279  
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<210> 282

<211> 61

<212> DNA

<213> Artificial Sequence

<220>

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<400> 282

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tgccaggtgg a 61

<210> 283

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<212> DNA

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<400> 283

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atgctgtgtg ccggctact 119

<210> 284

<211> 1875

<212> DNA

<213> Homo Sapien

<400> 284

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 gtaactgagg ccccatcctt ccgggcgact gaagcatcag actctaggaa 700  
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 ggctccacct tgcgtaacaa ctgaggtccc ttccattttg gcagctcaca 900  
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 caagggaact cctaccccat gccaggagg aggtgaggc tgaggctgag 1100  
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<210> 285

<211> 463

<212> PRT

<213> Homo Sapien

<400> 285

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|
| Met | His | Gly | Ser | Cys | Ser | Phe | Leu | Met | Leu | Leu | Leu | Pro | Leu | Leu |  |  |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |  |  |  |
| Leu | Leu | Leu | Val | Ala | Thr | Thr | Gly | Pro | Val | Gly | Ala | Leu | Thr | Asp |  |  |  |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |  |  |  |
| Glu | Glu | Lys | Arg | Leu | Met | Val | Glu | Leu | His | Asn | Leu | Tyr | Arg | Ala |  |  |  |
|     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |  |  |  |
| Gln | Val | Ser | Pro | Thr | Ala | Ser | Asp | Met | Leu | His | Met | Arg | Trp | Asp |  |  |  |
|     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |  |  |  |
| Glu | Glu | Leu | Ala | Ala | Phe | Ala | Lys | Ala | Tyr | Ala | Arg | Gln | Cys | Val |  |  |  |
|     |     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |  |  |  |
| Trp | Gly | His | Asn | Lys | Glu | Arg | Gly | Arg | Arg | Gly | Glu | Asn | Leu | Phe |  |  |  |
|     |     |     |     | 80  |     |     |     |     | 85  |     |     |     |     | 90  |  |  |  |
| Ala | Ile | Thr | Asp | Glu | Gly | Met | Asp | Val | Pro | Leu | Ala | Met | Glu | Glu |  |  |  |
|     |     |     |     | 95  |     |     |     |     | 100 |     |     |     |     | 105 |  |  |  |
| Trp | His | His | Glu | Arg | Glu | His | Tyr | Asn | Leu | Ser | Ala | Ala | Thr | Cys |  |  |  |
|     |     |     |     | 110 |     |     |     |     | 115 |     |     |     |     | 120 |  |  |  |
| Ser | Pro | Gly | Gln | Met | Cys | Gly | His | Tyr | Thr | Gln | Val | Val | Trp | Ala |  |  |  |
|     |     |     |     | 125 |     |     |     |     | 130 |     |     |     |     | 135 |  |  |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Thr | Glu | Arg | Ile | Gly | Cys | Gly | Ser | His | Phe | Cys | Glu | Lys | Leu | 140 | 145 | 150 |
| Gln | Gly | Val | Glu | Glu | Thr | Asn | Ile | Glu | Leu | Leu | Val | Cys | Asn | Tyr | 155 | 160 | 165 |
| Glu | Pro | Pro | Gly | Asn | Val | Lys | Gly | Lys | Arg | Pro | Tyr | Gln | Glu | Gly | 170 | 175 | 180 |
| Thr | Pro | Cys | Ser | Gln | Cys | Pro | Ser | Gly | Tyr | His | Cys | Lys | Asn | Ser | 185 | 190 | 195 |
| Leu | Cys | Glu | Pro | Ile | Gly | Ser | Pro | Glu | Asp | Ala | Gln | Asp | Leu | Pro | 200 | 205 | 210 |
| Tyr | Leu | Val | Thr | Glu | Ala | Pro | Ser | Phe | Arg | Ala | Thr | Glu | Ala | Ser | 215 | 220 | 225 |
| Asp | Ser | Arg | Lys | Met | Gly | Thr | Pro | Ser | Ser | Leu | Ala | Thr | Gly | Ile | 230 | 235 | 240 |
| Pro | Ala | Phe | Leu | Val | Thr | Glu | Val | Ser | Gly | Ser | Leu | Ala | Thr | Lys | 245 | 250 | 255 |
| Ala | Leu | Pro | Ala | Val | Glu | Thr | Gln | Ala | Pro | Thr | Ser | Leu | Ala | Thr | 260 | 265 | 270 |
| Lys | Asp | Pro | Pro | Ser | Met | Ala | Thr | Glu | Ala | Pro | Pro | Cys | Val | Thr | 275 | 280 | 285 |
| Thr | Glu | Val | Pro | Ser | Ile | Leu | Ala | Ala | His | Ser | Leu | Pro | Ser | Leu | 290 | 295 | 300 |
| Asp | Glu | Glu | Pro | Val | Thr | Phe | Pro | Lys | Ser | Thr | His | Val | Pro | Ile | 305 | 310 | 315 |
| Pro | Lys | Ser | Ala | Asp | Lys | Val | Thr | Asp | Lys | Thr | Lys | Val | Pro | Ser | 320 | 325 | 330 |
| Arg | Ser | Pro | Glu | Asn | Ser | Leu | Asp | Pro | Lys | Met | Ser | Leu | Thr | Gly | 335 | 340 | 345 |
| Ala | Arg | Glu | Leu | Leu | Pro | His | Ala | Gln | Glu | Glu | Ala | Glu | Ala | Glu | 350 | 355 | 360 |
| Ala | Glu | Leu | Pro | Pro | Ser | Ser | Glu | Val | Leu | Ala | Ser | Val | Phe | Pro | 365 | 370 | 375 |
| Ala | Gln | Asp | Lys | Pro | Gly | Glu | Leu | Gln | Ala | Thr | Leu | Asp | His | Thr | 380 | 385 | 390 |
| Gly | His | Thr | Ser | Ser | Lys | Ser | Leu | Pro | Asn | Phe | Pro | Asn | Thr | Ser | 395 | 400 | 405 |

09905056-07404

Ala Thr Ala Asn Ala Thr Gly Gly Arg Ala Leu Ala Leu Gln Ser  
410 415 420

Ser Leu Pro Gly Ala Glu Gly Pro Asp Lys Pro Ser Val Val Ser  
425 430 435

Gly Leu Asn Ser Gly Pro Gly His Val Trp Gly Pro Leu Leu Gly  
440 445 450

Leu Leu Leu Leu Pro Pro Leu Val Leu Ala Gly Ile Phe  
455 460

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<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 286

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<210> 287

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 287

ctcatattgc acaccagtaa ttcg 24

<210> 288

<211> 45

<212> DNA

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<400> 288

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<210> 289

<211> 3662

<212> DNA

<213> Homo Sapien

<400> 289

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 ctttttcaca ttagcagacc ggacttaagt cacaacagat tatctttcat 150  
 caaggcaagt tccatgagcc accttcaaag ccttcgagaa gtgaaactga 200  
 acaacaatga attggagacc attccaaatc tgggaccagt ctcggaat 250  
 attacacttc tctccttggc tggaaacagg attgttgaaa tactccctga 300  
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 gcccatcctc agctgctaaa aggaagaagc atttttgctg ttagcccaga 1350



tccttttgaa acatatcata caggttgcag tcctgaccca agaacagttt 2750  
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<211> 1059

<212> PRT

<213> Homo Sapien

<400> 290

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| Met | Val | Asp | Val | Leu | Leu | Leu | Phe | Ser | Leu | Cys | Leu | Leu | Phe | His |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Ser | Arg | Pro | Asp | Leu | Ser | His | Asn | Arg | Leu | Ser | Phe | Ile | Lys |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Ser | Ser | Met | Ser | His | Leu | Gln | Ser | Leu | Arg | Glu | Val | Lys | Leu | 35  | 40  | 45  |
| Asn | Asn | Asn | Glu | Leu | Glu | Thr | Ile | Pro | Asn | Leu | Gly | Pro | Val | Ser | 50  | 55  | 60  |
| Ala | Asn | Ile | Thr | Leu | Leu | Ser | Leu | Ala | Gly | Asn | Arg | Ile | Val | Glu | 65  | 70  | 75  |
| Ile | Leu | Pro | Glu | His | Leu | Lys | Glu | Phe | Gln | Ser | Leu | Glu | Thr | Leu | 80  | 85  | 90  |
| Asp | Leu | Ser | Ser | Asn | Asn | Ile | Ser | Glu | Leu | Gln | Thr | Ala | Phe | Pro | 95  | 100 | 105 |
| Ala | Leu | Gln | Leu | Lys | Tyr | Leu | Tyr | Leu | Asn | Ser | Asn | Arg | Val | Thr | 110 | 115 | 120 |
| Ser | Met | Glu | Pro | Gly | Tyr | Phe | Asp | Asn | Leu | Ala | Asn | Thr | Leu | Leu | 125 | 130 | 135 |
| Val | Leu | Lys | Leu | Asn | Arg | Asn | Arg | Ile | Ser | Ala | Ile | Pro | Pro | Lys | 140 | 145 | 150 |
| Met | Phe | Lys | Leu | Pro | Gln | Leu | Gln | His | Leu | Glu | Leu | Asn | Arg | Asn | 155 | 160 | 165 |
| Lys | Ile | Lys | Asn | Val | Asp | Gly | Leu | Thr | Phe | Gln | Gly | Leu | Gly | Ala | 170 | 175 | 180 |
| Leu | Lys | Ser | Leu | Lys | Met | Gln | Arg | Asn | Gly | Val | Thr | Lys | Leu | Met | 185 | 190 | 195 |
| Asp | Gly | Ala | Phe | Trp | Gly | Leu | Ser | Asn | Met | Glu | Ile | Leu | Gln | Leu | 200 | 205 | 210 |
| Asp | His | Asn | Asn | Leu | Thr | Glu | Ile | Thr | Lys | Gly | Trp | Leu | Tyr | Gly | 215 | 220 | 225 |
| Leu | Leu | Met | Leu | Gln | Glu | Leu | His | Leu | Ser | Gln | Asn | Ala | Ile | Asn | 230 | 235 | 240 |
| Arg | Ile | Ser | Pro | Asp | Ala | Trp | Glu | Phe | Cys | Gln | Lys | Leu | Ser | Glu | 245 | 250 | 255 |
| Leu | Asp | Leu | Thr | Phe | Asn | His | Leu | Ser | Arg | Leu | Asp | Asp | Ser | Ser | 260 | 265 | 270 |
| Phe | Leu | Gly | Leu | Ser | Leu | Leu | Asn | Thr | Leu | His | Ile | Gly | Asn | Asn | 275 | 280 | 285 |
| Arg | Val | Ser | Tyr | Ile | Ala | Asp | Cys | Ala | Phe | Arg | Gly | Leu | Ser | Ser |     |     |     |

09905056-071001



|   |     |  |     |  |     |
|---|-----|--|-----|--|-----|
|   | 290 |  | 295 |  | 300 |
| Leu Lys Thr Leu Asp Leu Lys Asn Asn Glu Ile Ser Trp Thr Ile | 305 |  | 310 |  | 315 |
| Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg | 320 |  | 325 |  | 330 |
| Leu Ile Leu Gln Gly Asn Arg Ile Arg Ser Ile Thr Lys Lys Ala | 335 |  | 340 |  | 345 |
| Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn | 350 |  | 355 |  | 360 |
| Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys | 365 |  | 370 |  | 375 |
| Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys | 380 |  | 385 |  | 390 |
| Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln | 395 |  | 400 |  | 405 |
| Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly | 410 |  | 415 |  | 420 |
| Arg Ser Ile Phe Ala Val Ser Pro Asp Gly Phe Val Cys Asp Asp | 425 |  | 430 |  | 435 |
| Phe Pro Lys Pro Gln Ile Thr Val Gln Pro Glu Thr Gln Ser Ala | 440 |  | 445 |  | 450 |
| Ile Lys Gly Ser Asn Leu Ser Phe Ile Cys Ser Ala Ala Ser Ser | 455 |  | 460 |  | 465 |
| Ser Asp Ser Pro Met Thr Phe Ala Trp Lys Lys Asp Asn Glu Leu | 470 |  | 475 |  | 480 |
| Leu His Asp Ala Glu Met Glu Asn Tyr Ala His Leu Arg Ala Gln | 485 |  | 490 |  | 495 |
| Gly Gly Glu Val Met Glu Tyr Thr Thr Ile Leu Arg Leu Arg Glu | 500 |  | 505 |  | 510 |
| Val Glu Phe Ala Ser Glu Gly Lys Tyr Gln Cys Val Ile Ser Asn | 515 |  | 520 |  | 525 |
| His Phe Gly Ser Ser Tyr Ser Val Lys Ala Lys Leu Thr Val Asn | 530 |  | 535 |  | 540 |
| Met Leu Pro Ser Phe Thr Lys Thr Pro Met Asp Leu Thr Ile Arg | 545 |  | 550 |  | 555 |

09905055-074204

|                 |                     |                     |     |
|-----------------|---------------------|---------------------|-----|
| Ala Gly Ala Met | Ala Arg Leu Glu Cys | Ala Ala Val Gly His | Pro |
| 560             | 565                 |                     | 570 |
| Ala Pro Gln Ile | Ala Trp Gln Lys Asp | Gly Gly Thr Asp Phe | Pro |
| 575             | 580                 |                     | 585 |
| Ala Ala Arg Glu | Arg Arg Met His Val | Met Pro Glu Asp Asp | Val |
| 590             | 595                 |                     | 600 |
| Phe Phe Ile Val | Asp Val Lys Ile Glu | Asp Ile Gly Val Tyr | Ser |
| 605             | 610                 |                     | 615 |
| Cys Thr Ala Gln | Asn Ser Ala Gly Ser | Ile Ser Ala Asn Ala | Thr |
| 620             | 625                 |                     | 630 |
| Leu Thr Val Leu | Glu Thr Pro Ser Phe | Leu Arg Pro Leu Leu | Asp |
| 635             | 640                 |                     | 645 |
| Arg Thr Val Thr | Lys Gly Glu Thr Ala | Val Leu Gln Cys Ile | Ala |
| 650             | 655                 |                     | 660 |
| Gly Gly Ser Pro | Pro Pro Lys Leu Asn | Trp Thr Lys Asp Asp | Ser |
| 665             | 670                 |                     | 675 |
| Pro Leu Val Val | Thr Glu Arg His Phe | Phe Ala Ala Gly Asn | Gln |
| 680             | 685                 |                     | 690 |
| Leu Leu Ile Ile | Val Asp Ser Asp Val | Ser Asp Ala Gly Lys | Tyr |
| 695             | 700                 |                     | 705 |
| Thr Cys Glu Met | Ser Asn Thr Leu Gly | Thr Glu Arg Gly Asn | Val |
| 710             | 715                 |                     | 720 |
| Arg Leu Ser Val | Ile Pro Thr Pro Thr | Cys Asp Ser Pro Gln | Met |
| 725             | 730                 |                     | 735 |
| Thr Ala Pro Ser | Leu Asp Asp Asp Gly | Trp Ala Thr Val Gly | Val |
| 740             | 745                 |                     | 750 |
| Val Ile Ile Ala | Val Val Cys Cys Val | Val Gly Thr Ser Leu | Val |
| 755             | 760                 |                     | 765 |
| Trp Val Val Ile | Ile Tyr His Thr Arg | Arg Arg Asn Glu Asp | Cys |
| 770             | 775                 |                     | 780 |
| Ser Ile Thr Asn | Thr Asp Glu Thr Asn | Leu Pro Ala Asp Ile | Pro |
| 785             | 790                 |                     | 795 |
| Ser Tyr Leu Ser | Ser Gln Gly Thr Leu | Ala Asp Arg Gln Asp | Gly |
| 800             | 805                 |                     | 810 |

09905056-074304

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |      |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|
| Tyr | Val | Ser | Ser | Glu | Ser | Gly | Ser | His | His | Gln | Phe | Val | Thr | Ser | 815  | 820  | 825  |
| Ser | Gly | Ala | Gly | Phe | Phe | Leu | Pro | Gln | His | Asp | Ser | Ser | Gly | Thr | 830  | 835  | 840  |
| Cys | His | Ile | Asp | Asn | Ser | Ser | Glu | Ala | Asp | Val | Glu | Ala | Ala | Thr | 845  | 850  | 855  |
| Asp | Leu | Phe | Leu | Cys | Pro | Phe | Leu | Gly | Ser | Thr | Gly | Pro | Met | Tyr | 860  | 865  | 870  |
| Leu | Lys | Gly | Asn | Val | Tyr | Gly | Ser | Asp | Pro | Phe | Glu | Thr | Tyr | His | 875  | 880  | 885  |
| Thr | Gly | Cys | Ser | Pro | Asp | Pro | Arg | Thr | Val | Leu | Met | Asp | His | Tyr | 890  | 895  | 900  |
| Glu | Pro | Ser | Tyr | Ile | Lys | Lys | Lys | Glu | Cys | Tyr | Pro | Cys | Ser | His | 905  | 910  | 915  |
| Pro | Ser | Glu | Glu | Ser | Cys | Glu | Arg | Ser | Phe | Ser | Asn | Ile | Ser | Trp | 920  | 925  | 930  |
| Pro | Ser | His | Val | Arg | Lys | Leu | Leu | Asn | Thr | Ser | Tyr | Ser | His | Asn | 935  | 940  | 945  |
| Glu | Gly | Pro | Gly | Met | Lys | Asn | Leu | Cys | Leu | Asn | Lys | Ser | Ser | Leu | 950  | 955  | 960  |
| Asp | Phe | Ser | Ala | Asn | Pro | Glu | Pro | Ala | Ser | Val | Ala | Ser | Ser | Asn | 965  | 970  | 975  |
| Ser | Phe | Met | Gly | Thr | Phe | Gly | Lys | Ala | Leu | Arg | Arg | Pro | His | Leu | 980  | 985  | 990  |
| Asp | Ala | Tyr | Ser | Ser | Phe | Gly | Gln | Pro | Ser | Asp | Cys | Gln | Pro | Arg | 995  | 1000 | 1005 |
| Ala | Phe | Tyr | Leu | Lys | Ala | His | Ser | Ser | Pro | Asp | Leu | Asp | Ser | Gly | 1010 | 1015 | 1020 |
| Ser | Glu | Glu | Asp | Gly | Lys | Glu | Arg | Thr | Asp | Phe | Gln | Glu | Glu | Asn | 1025 | 1030 | 1035 |
| His | Ile | Cys | Thr | Phe | Lys | Gln | Thr | Leu | Glu | Asn | Tyr | Arg | Thr | Pro | 1040 | 1045 | 1050 |
| Asn | Phe | Gln | Ser | Tyr | Asp | Leu | Asp | Thr |     |     |     |     |     |     | 1055 |      |      |

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&lt;211&gt; 2906

09905056 071201

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 291

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<212> PRT

<213> Homo Sapien

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Asn | Lys | Met | Thr | Leu | His | Pro | Gln | Gln | Ile | Met | Ile | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |
| Pro | Arg | Phe | Asn | Arg | Ala | Leu | Phe | Asp | Pro | Leu | Leu | Val | Val | Leu |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |
| Leu | Ala | Leu | Gln | Leu | Leu | Val | Val | Ala | Gly | Leu | Val | Arg | Ala | Gln |
|     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |
| Thr | Cys | Pro | Ser | Val | Cys | Ser | Cys | Ser | Asn | Gln | Phe | Ser | Lys | Val |
|     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |
| Ile | Cys | Val | Arg | Lys | Asn | Leu | Arg | Glu | Val | Pro | Asp | Gly | Ile | Ser |
|     |     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |
| Thr | Asn | Thr | Arg | Leu | Leu | Asn | Leu | His | Glu | Asn | Gln | Ile | Gln | Ile |
|     |     |     |     | 80  |     |     |     |     | 85  |     |     |     |     | 90  |
| Ile | Lys | Val | Asn | Ser | Phe | Lys | His | Leu | Arg | His | Leu | Glu | Ile | Leu |
|     |     |     |     | 95  |     |     |     |     | 100 |     |     |     |     | 105 |
| Gln | Leu | Ser | Arg | Asn | His | Ile | Arg | Thr | Ile | Glu | Ile | Gly | Ala | Phe |
|     |     |     |     | 110 |     |     |     |     | 115 |     |     |     |     | 120 |
| Asn | Gly | Leu | Ala | Asn | Leu | Asn | Thr | Leu | Glu | Leu | Phe | Asp | Asn | Arg |
|     |     |     |     | 125 |     |     |     |     | 130 |     |     |     |     | 135 |
| Leu | Thr | Thr | Ile | Pro | Asn | Gly | Ala | Phe | Val | Tyr | Leu | Ser | Lys | Leu |
|     |     |     |     | 140 |     |     |     |     | 145 |     |     |     |     | 150 |
| Lys | Glu | Leu | Trp | Leu | Arg | Asn | Asn | Pro | Ile | Glu | Ser | Ile | Pro | Ser |

|   |     |  |     |  |     |
|---|-----|--|-----|--|-----|
|   | 155 |  | 160 |  | 165 |
| Tyr Ala Phe Asn Arg Ile Pro Ser Leu Arg Arg Leu Asp Leu Gly | 170 |  | 175 |  | 180 |
| Glu Leu Lys Arg Leu Ser Tyr Ile Ser Glu Gly Ala Phe Glu Gly | 185 |  | 190 |  | 195 |
| Leu Ser Asn Leu Arg Tyr Leu Asn Leu Ala Met Cys Asn Leu Arg | 200 |  | 205 |  | 210 |
| Glu Ile Pro Asn Leu Thr Pro Leu Ile Lys Leu Asp Glu Leu Asp | 215 |  | 220 |  | 225 |
| Leu Ser Gly Asn His Leu Ser Ala Ile Arg Pro Gly Ser Phe Gln | 230 |  | 235 |  | 240 |
| Gly Leu Met His Leu Gln Lys Leu Trp Met Ile Gln Ser Gln Ile | 245 |  | 250 |  | 255 |
| Gln Val Ile Glu Arg Asn Ala Phe Asp Asn Leu Gln Ser Leu Val | 260 |  | 265 |  | 270 |
| Glu Ile Asn Leu Ala His Asn Asn Leu Thr Leu Leu Pro His Asp | 275 |  | 280 |  | 285 |
| Leu Phe Thr Pro Leu His His Leu Glu Arg Ile His Leu His His | 290 |  | 295 |  | 300 |
| Asn Pro Trp Asn Cys Asn Cys Asp Ile Leu Trp Leu Ser Trp Trp | 305 |  | 310 |  | 315 |
| Ile Lys Asp Met Ala Pro Ser Asn Thr Ala Cys Cys Ala Arg Cys | 320 |  | 325 |  | 330 |
| Asn Thr Pro Pro Asn Leu Lys Gly Arg Tyr Ile Gly Glu Leu Asp | 335 |  | 340 |  | 345 |
| Gln Asn Tyr Phe Thr Cys Tyr Ala Pro Val Ile Val Glu Pro Pro | 350 |  | 355 |  | 360 |
| Ala Asp Leu Asn Val Thr Glu Gly Met Ala Ala Glu Leu Lys Cys | 365 |  | 370 |  | 375 |
| Arg Ala Ser Thr Ser Leu Thr Ser Val Ser Trp Ile Thr Pro Asn | 380 |  | 385 |  | 390 |
| Gly Thr Val Met Thr His Gly Ala Tyr Lys Val Arg Ile Ala Val | 395 |  | 400 |  | 405 |
| Leu Ser Asp Gly Thr Leu Asn Phe Thr Asn Val Thr Val Gln Asp | 410 |  | 415 |  | 420 |

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 Val Asp Asp Glu Ile Thr Gly Asp Thr Pro Met Glu Ser His Leu  
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 Pro Met Pro Ala Ile Glu His Glu His Leu Asn His Tyr Asn Ser  
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 Tyr Lys Ser Pro Phe Asn His Thr Thr Thr Val Asn Thr Ile Asn  
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|                                     |                         |  |     |  |     |
|-------------------------------------|-------------------------|--|-----|--|-----|
|                                     | 215                     |  | 220 |  | 225 |
| Lys Ile Lys Asn Val Asp Gly Leu Thr | Phe Gln Gly Leu Gly Ala |  |     |  |     |
| 230                                 | 235                     |  |     |  | 240 |
| Leu Lys Ser Leu Lys Met Gln Arg Asn | Gly Val Thr Lys Leu Met |  |     |  |     |
| 245                                 | 250                     |  |     |  | 255 |
| Asp Gly Ala Phe Trp Gly Leu Ser Asn | Met Glu Ile Leu Gln Leu |  |     |  |     |
| 260                                 | 265                     |  |     |  | 270 |
| Asp His Asn Asn Leu Thr Glu Ile Thr | Lys Gly Trp Leu Tyr Gly |  |     |  |     |
| 275                                 | 280                     |  |     |  | 285 |
| Leu Leu Met Leu Gln Glu Leu His Leu | Ser Gln Asn Ala Ile Asn |  |     |  |     |
| 290                                 | 295                     |  |     |  | 300 |
| Arg Ile Ser Pro Asp Ala Trp Glu Phe | Cys Gln Lys Leu Ser Glu |  |     |  |     |
| 305                                 | 310                     |  |     |  | 315 |
| Leu Asp Leu Thr Phe Asn His Leu Ser | Arg Leu Asp Asp Ser Ser |  |     |  |     |
| 320                                 | 325                     |  |     |  | 330 |
| Phe Leu Gly Leu Ser Leu Leu Asn Thr | Leu His Ile Gly Asn Asn |  |     |  |     |
| 335                                 | 340                     |  |     |  | 345 |
| Arg Val Ser Tyr Ile Ala Asp Cys Ala | Phe Arg Gly Leu Ser Ser |  |     |  |     |
| 350                                 | 355                     |  |     |  | 360 |
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| 365                                 | 370                     |  |     |  | 375 |
| Glu Asp Met Asn Gly Ala Phe Ser Gly | Leu Asp Lys Leu Arg Arg |  |     |  |     |
| 380                                 | 385                     |  |     |  | 390 |
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| 410                                 | 415                     |  |     |  | 420 |
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| 425                                 | 430                     |  |     |  | 435 |
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| 440                                 | 445                     |  |     |  | 450 |
| Gln Leu Lys Trp Leu Pro Gln Trp Val | Ala Glu Asn Asn Phe Gln |  |     |  |     |
| 455                                 | 460                     |  |     |  | 465 |
| Ser Phe Val Asn Ala Ser Cys Ala His | Pro Gln Leu Leu Lys Gly |  |     |  |     |
| 470                                 | 475                     |  |     |  | 480 |

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ser | Ile | Phe | Ala | Val | Ser | Pro | Asp | Gly | Phe | Val | Cys | Asp | Asp |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |
| Phe | Pro | Lys | Pro | Gln | Ile | Thr | Val | Gln | Pro | Glu | Thr | Gln | Ser | Ala |
|     |     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |
| Ile | Lys | Gly | Ser | Asn | Leu | Ser | Phe | Ile | Cys | Ser | Ala | Ala | Ser | Ser |
|     |     |     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |
| Ser | Asp | Ser | Pro | Met | Thr | Phe | Ala | Trp | Lys | Lys | Asp | Asn | Glu | Leu |
|     |     |     |     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |
| Leu | His | Asp | Ala | Glu | Met | Glu | Asn | Tyr | Ala | His | Leu | Arg | Ala | Gln |
|     |     |     |     | 545 |     |     |     |     | 550 |     |     |     |     | 555 |
| Gly | Gly | Glu | Val | Met | Glu | Tyr | Thr | Thr | Ile | Leu | Arg | Leu | Arg | Glu |
|     |     |     |     | 560 |     |     |     |     | 565 |     |     |     |     | 570 |
| Val | Glu | Phe | Ala | Ser | Glu | Gly | Lys | Tyr | Gln | Cys | Val | Ile | Ser | Asn |
|     |     |     |     | 575 |     |     |     |     | 580 |     |     |     |     | 585 |
| His | Phe | Gly | Ser | Ser | Tyr | Ser | Val | Lys | Ala | Lys | Leu | Thr | Val | Asn |
|     |     |     |     | 590 |     |     |     |     | 595 |     |     |     |     | 600 |
| Met | Leu | Pro | Ser | Phe | Thr | Lys | Thr | Pro | Met | Asp | Leu | Thr | Ile | Arg |
|     |     |     |     | 605 |     |     |     |     | 610 |     |     |     |     | 615 |
| Ala | Gly | Ala | Met | Ala | Arg | Leu | Glu | Cys | Ala | Ala | Val | Gly | His | Pro |
|     |     |     |     | 620 |     |     |     |     | 625 |     |     |     |     | 630 |
| Ala | Pro | Gln | Ile | Ala | Trp | Gln | Lys | Asp | Gly | Gly | Thr | Asp | Phe | Pro |
|     |     |     |     | 635 |     |     |     |     | 640 |     |     |     |     | 645 |
| Ala | Ala | Arg | Glu | Arg | Arg | Met | His | Val | Met | Pro | Glu | Asp | Asp | Val |
|     |     |     |     | 650 |     |     |     |     | 655 |     |     |     |     | 660 |
| Phe | Phe | Ile | Val | Asp | Val | Lys | Ile | Glu | Asp | Ile | Gly | Val | Tyr | Ser |
|     |     |     |     | 665 |     |     |     |     | 670 |     |     |     |     | 675 |
| Cys | Thr | Ala | Gln | Asn | Ser | Ala | Gly | Ser | Ile | Ser | Ala | Asn | Ala | Thr |
|     |     |     |     | 680 |     |     |     |     | 685 |     |     |     |     | 690 |
| Leu | Thr | Val | Leu | Glu | Thr | Pro | Ser | Phe | Leu | Arg | Pro | Leu | Leu | Asp |
|     |     |     |     | 695 |     |     |     |     | 700 |     |     |     |     | 705 |
| Arg | Thr | Val | Thr | Lys | Gly | Glu | Thr | Ala | Val | Leu | Gln | Cys | Ile | Ala |
|     |     |     |     | 710 |     |     |     |     | 715 |     |     |     |     | 720 |
| Gly | Gly | Ser | Pro | Pro | Pro | Lys | Leu | Asn | Trp | Thr | Lys | Asp | Asp | Ser |
|     |     |     |     | 725 |     |     |     |     | 730 |     |     |     |     | 735 |
| Pro | Leu | Val | Val | Thr | Glu | Arg | His | Phe | Phe | Ala | Ala | Gly | Asn | Gln |
|     |     |     |     | 740 |     |     |     |     | 745 |     |     |     |     | 750 |

|     |     |     |     |     |     |     |     |     |      |     |     |     |     |      |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|--|
| Leu | Leu | Ile | Ile | Val | Asp | Ser | Asp | Val | Ser  | Asp | Ala | Gly | Lys | Tyr  |  |
|     |     |     |     | 755 |     |     |     |     | 760  |     |     |     |     | 765  |  |
| Thr | Cys | Glu | Met | Ser | Asn | Thr | Leu | Gly | Thr  | Glu | Arg | Gly | Asn | Val  |  |
|     |     |     |     | 770 |     |     |     |     | 775  |     |     |     |     | 780  |  |
| Arg | Leu | Ser | Val | Ile | Pro | Thr | Pro | Thr | Cys  | Asp | Ser | Pro | Gln | Met  |  |
|     |     |     |     | 785 |     |     |     |     | 790  |     |     |     |     | 795  |  |
| Thr | Ala | Pro | Ser | Leu | Asp | Asp | Asp | Gly | Trp  | Ala | Thr | Val | Gly | Val  |  |
|     |     |     |     | 800 |     |     |     |     | 805  |     |     |     |     | 810  |  |
| Val | Ile | Ile | Ala | Val | Val | Cys | Cys | Val | Val  | Gly | Thr | Ser | Leu | Val  |  |
|     |     |     |     | 815 |     |     |     |     | 820  |     |     |     |     | 825  |  |
| Trp | Val | Val | Ile | Ile | Tyr | His | Thr | Arg | Arg  | Arg | Asn | Glu | Asp | Cys  |  |
|     |     |     |     | 830 |     |     |     |     | 835  |     |     |     |     | 840  |  |
| Ser | Ile | Thr | Asn | Thr | Asp | Glu | Thr | Asn | Leu  | Pro | Ala | Asp | Ile | Pro  |  |
|     |     |     |     | 845 |     |     |     |     | 850  |     |     |     |     | 855  |  |
| Ser | Tyr | Leu | Ser | Ser | Gln | Gly | Thr | Leu | Ala  | Asp | Arg | Gln | Asp | Gly  |  |
|     |     |     |     | 860 |     |     |     |     | 865  |     |     |     |     | 870  |  |
| Tyr | Val | Ser | Ser | Glu | Ser | Gly | Ser | His | His  | Gln | Phe | Val | Thr | Ser  |  |
|     |     |     |     | 875 |     |     |     |     | 880  |     |     |     |     | 885  |  |
| Ser | Gly | Ala | Gly | Phe | Phe | Leu | Pro | Gln | His  | Asp | Ser | Ser | Gly | Thr  |  |
|     |     |     |     | 890 |     |     |     |     | 895  |     |     |     |     | 900  |  |
| Cys | His | Ile | Asp | Asn | Ser | Ser | Glu | Ala | Asp  | Val | Glu | Ala | Ala | Thr  |  |
|     |     |     |     | 905 |     |     |     |     | 910  |     |     |     |     | 915  |  |
| Asp | Leu | Phe | Leu | Cys | Pro | Phe | Leu | Gly | Ser  | Thr | Gly | Pro | Met | Tyr  |  |
|     |     |     |     | 920 |     |     |     |     | 925  |     |     |     |     | 930  |  |
| Leu | Lys | Gly | Asn | Val | Tyr | Gly | Ser | Asp | Pro  | Phe | Glu | Thr | Tyr | His  |  |
|     |     |     |     | 935 |     |     |     |     | 940  |     |     |     |     | 945  |  |
| Thr | Gly | Cys | Ser | Pro | Asp | Pro | Arg | Thr | Val  | Leu | Met | Asp | His | Tyr  |  |
|     |     |     |     | 950 |     |     |     |     | 955  |     |     |     |     | 960  |  |
| Glu | Pro | Ser | Tyr | Ile | Lys | Lys | Lys | Glu | Cys  | Tyr | Pro | Cys | Ser | His  |  |
|     |     |     |     | 965 |     |     |     |     | 970  |     |     |     |     | 975  |  |
| Pro | Ser | Glu | Glu | Ser | Cys | Glu | Arg | Ser | Phe  | Ser | Asn | Ile | Ser | Trp  |  |
|     |     |     |     | 980 |     |     |     |     | 985  |     |     |     |     | 990  |  |
| Pro | Ser | His | Val | Arg | Lys | Leu | Leu | Asn | Thr  | Ser | Tyr | Ser | His | Asn  |  |
|     |     |     |     | 995 |     |     |     |     | 1000 |     |     |     |     | 1005 |  |
| Glu | Gly | Pro | Gly | Met | Lys | Asn | Leu | Cys | Leu  | Asn | Lys | Ser | Ser | Leu  |  |

|   |      |      |
|---|------|------|
| 1010  | 1015 | 1020 |
| Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn |      |      |
| 1025  | 1030 | 1035 |
| Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu |      |      |
| 1040  | 1045 | 1050 |
| Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg |      |      |
| 1055  | 1060 | 1065 |
| Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly |      |      |
| 1070  | 1075 | 1080 |
| Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn |      |      |
| 1085  | 1090 | 1095 |
| His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro |      |      |
| 1100  | 1105 | 1110 |
| Asn Phe Gln Ser Tyr Asp Leu Asp Thr                         |      |      |
| 1115  |      |      |

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 ggcgcgctcg ggcgcggggc gcagcaggga aggggaagct gtggtctgcc 150  
 ctgctccacg aggcgcact ggtgtgaacc gggagagccc ctgggtggtc 200  
 ccgtccccta tccctccttt atatagaaac cttccacact ggggaaggcag 250  
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| Met | Asp | Phe | Leu | Leu | Ala | Leu | Val | Leu | Val | Ser | Ser | Leu | Tyr | Leu | 1   | 5   | 10  | 15 |
| Gln | Ala | Ala | Ala | Glu | Phe | Asp | Gly | Arg | Trp | Pro | Arg | Gln | Ile | Val | 20  | 25  | 30  |    |
| Ser | Ser | Ile | Gly | Leu | Cys | Arg | Tyr | Gly | Gly | Arg | Ile | Asp | Cys | Cys | 35  | 40  | 45  |    |
| Trp | Gly | Trp | Ala | Arg | Gln | Ser | Trp | Gly | Gln | Cys | Gln | Pro | Val | Cys | 50  | 55  | 60  |    |
| Gln | Pro | Arg | Cys | Lys | His | Gly | Glu | Cys | Ile | Gly | Pro | Asn | Lys | Cys | 65  | 70  | 75  |    |
| Lys | Cys | His | Pro | Gly | Tyr | Ala | Gly | Lys | Thr | Cys | Asn | Gln | Asp | Leu | 80  | 85  | 90  |    |
| Asn | Glu | Cys | Gly | Leu | Lys | Pro | Arg | Pro | Cys | Lys | His | Arg | Cys | Met | 95  | 100 | 105 |    |
| Asn | Thr | Tyr | Gly | Ser | Tyr | Lys | Cys | Tyr | Cys | Leu | Asn | Gly | Tyr | Met | 110 | 115 | 120 |    |
| Leu | Met | Pro | Asp | Gly | Ser | Cys | Ser | Ser | Ala | Leu | Thr | Cys | Ser | Met | 125 | 130 | 135 |    |
| Ala | Asn | Cys | Gln | Tyr | Gly | Cys | Asp | Val | Val | Lys | Gly | Gln | Ile | Arg | 140 | 145 | 150 |    |
| Cys | Gln | Cys | Pro | Ser | Pro | Gly | Leu | His | Leu | Ala | Pro | Asp | Gly | Arg | 155 | 160 | 165 |    |

|                 |                     |                         |
|-----------------|---------------------|-------------------------|
| Thr Cys Val Asp | Val Asp Glu Cys Ala | Thr Gly Arg Ala Ser Cys |
| 170             | 175                 | 180                     |
| Pro Arg Phe Arg | Gln Cys Val Asn Thr | Phe Gly Ser Tyr Ile Cys |
| 185             | 190                 | 195                     |
| Lys Cys His Lys | Gly Phe Asp Leu Met | Tyr Ile Gly Gly Lys Tyr |
| 200             | 205                 | 210                     |
| Gln Cys His Asp | Ile Asp Glu Cys Ser | Leu Gly Gln Tyr Gln Cys |
| 215             | 220                 | 225                     |
| Ser Ser Phe Ala | Arg Cys Tyr Asn Val | Arg Gly Ser Tyr Lys Cys |
| 230             | 235                 | 240                     |
| Lys Cys Lys Glu | Gly Tyr Gln Gly Asp | Gly Leu Thr Cys Val Tyr |
| 245             | 250                 | 255                     |
| Ile Pro Lys Val | Met Ile Glu Pro Ser | Gly Pro Ile His Val Pro |
| 260             | 265                 | 270                     |
| Lys Gly Asn Gly | Thr Ile Leu Lys Gly | Asp Thr Gly Asn Asn Asn |
| 275             | 280                 | 285                     |
| Trp Ile Pro Asp | Val Gly Ser Thr Trp | Trp Pro Pro Lys Thr Pro |
| 290             | 295                 | 300                     |
| Tyr Ile Pro Pro | Ile Ile Thr Asn Arg | Pro Thr Ser Lys Pro Thr |
| 305             | 310                 | 315                     |
| Thr Arg Pro Thr | Pro Lys Pro Thr Pro | Ile Pro Thr Pro Pro Pro |
| 320             | 325                 | 330                     |
| Pro Pro Pro Leu | Pro Thr Glu Leu Arg | Thr Pro Leu Pro Pro Thr |
| 335             | 340                 | 345                     |
| Thr Pro Glu Arg | Pro Thr Thr Gly Leu | Thr Thr Ile Ala Pro Ala |
| 350             | 355                 | 360                     |
| Ala Ser Thr Pro | Pro Gly Gly Ile Thr | Val Asp Asn Arg Val Gln |
| 365             | 370                 | 375                     |
| Thr Asp Pro Gln | Lys Pro Arg Gly Asp | Val Phe Ser Val Leu Val |
| 380             | 385                 | 390                     |
| His Ser Cys Asn | Phe Asp His Gly Leu | Cys Gly Trp Ile Arg Glu |
| 395             | 400                 | 405                     |
| Lys Asp Asn Asp | Leu His Trp Glu Pro | Ile Arg Asp Pro Ala Gly |
| 410             | 415                 | 420                     |
| Gly Gln Tyr Leu | Thr Val Ser Ala Ala | Lys Ala Pro Gly Gly Lys |

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|   |     |  |     |  |     |
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|   | 440 |  | 445 |  | 450 |
| Asp Leu Cys Leu Ser Phe Arg His Lys Val Thr Gly Leu His Ser |     |  |     |  |     |
|   | 455 |  | 460 |  | 465 |
| Gly Thr Leu Gln Val Phe Val Arg Lys His Gly Ala His Gly Ala |     |  |     |  |     |
|   | 470 |  | 475 |  | 480 |
| Ala Leu Trp Gly Arg Asn Gly Gly His Gly Trp Arg Gln Thr Gln |     |  |     |  |     |
|   | 485 |  | 490 |  | 495 |
| Ile Thr Leu Arg Gly Ala Asp Ile Lys Ser Glu Ser Gln Arg     |     |  |     |  |     |
|   | 500 |  | 505 |  |     |

&lt;210&gt; 316

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 316

gatggttcct gctcaagtgc cctg 24

&lt;210&gt; 317

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 317

ttgcacttgt aggaccacg tacg 24

&lt;210&gt; 318

&lt;211&gt; 50

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 318

ctgatgggag gacctgtgta gatgttgatg aatgtgctac aggaagagcc 50

&lt;210&gt; 319

&lt;211&gt; 2110

&lt;212&gt; DNA

F03T40"95050660

&lt;213&gt; Homo Sapien

&lt;400&gt; 319

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 ttttagattgt gaaatgtggc tcaaggtctt cacaactttc ctttcctttg 100  
 caacaggtgc ttgctcgggg ctgaaggtga cagtgccatc acacactgtc 150  
 catggcgta gaggtcaggc cctctaccta cccgtccact atggcttcca 200  
 cactccagca tcagacatcc agatcatatg gctatttgag agaccccaca 250  
 caatgcccac atacttactg ggctctgtga ataagtctgt ggttcctgac 300  
 ttggaatacc aacacaagtt caccatgatg ccaccaatg catctctgct 350  
 tatcaaccca ctgcagttcc ctgatgaagg caattacatc gtgaaggtca 400  
 acattcaggg aaatggaact ctatctgcca gtcagaagat acaagtcacg 450  
 gttgatgatc ctgtcacaaa gccagtggtg cagattcacc ctccctctgg 500  
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 tcagtgaat ggaaagtgat atcattatgc ccatcatata ttatggacct 750  
 tatggacttc aagtgaattc tgataaaggg ctaaaagtag gggaaagtgt 800  
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 aatcagtga gaaaccagga ccaacacctc ttactcatta ttcttttaca 1550  
 tgcagaatag aggcatttat gcaaattgaa ctgcagggtt ttcagcatat 1600  
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 ggagagtcgt tctcatgctg acggggagaa cgaaagtgaac aggggtttcc 1700  
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 tttattagt ttaagaatgc taaatttatg tttcaatttt atttccaaat 1900  
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 aaaaaactat gccttctctt ttttttcaat caccagtagt atttttgaga 2000  
 agacttgtga acacttaagg aaatgactat taaagtctta tttttatttt 2050  
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 aaaaaaaaaa 2110

<210> 320

<211> 450

<212> PRT

<213> Homo Sapien

<400> 320

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Trp | Leu | Lys | Val | Phe | Thr | Thr | Phe | Leu | Ser | Phe | Ala | Thr | Gly |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Cys | Ser | Gly | Leu | Lys | Val | Thr | Val | Pro | Ser | His | Thr | Val | His |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Val | Arg | Gly | Gln | Ala | Leu | Tyr | Leu | Pro | Val | His | Tyr | Gly | Phe |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Thr | Pro | Ala | Ser | Asp | Ile | Gln | Ile | Ile | Trp | Leu | Phe | Glu | Arg |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |





<220>

<223> Synthetic Oligonucleotide Probe

<400> 323

ctccctctgg gctgtggagt atgtggggaa catgaccctg acatg 45

<210> 324

<211> 2397

<212> DNA

<213> Homo Sapien

<400> 324

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 cctggtgctg ttgctttggg gtgctccctg gacgcacggg cggcggagca 100  
 acgttcgcgt catcacggac gagaactgga gagaactgct ggaaggagac 150  
 tggatgatag aattttatgc ccctggtgct cctgcttgct aaaatcttca 200  
 accggaatgg gaaagttttg ctgaatgggg agaagatctt gaggttaata 250  
 ttgcgaaagt agatgtcaca gacgagccag gactgagtgg acggtttatc 300  
 ataactgctc ttctactat ttatcattgt aaagatgggt aatttaggcg 350  
 ctatcagggt ccaaggacta agaaggactt cataaaacttt ataagtgata 400  
 aagagtggaa gagtattgag ccggtttcat catgggttgg tccaggttct 450  
 gttctgatga gtagtatgtc agcactcttt cagctatcta tgtggatcag 500  
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 catatactgt ttttgcttta gcaactctgt tttccggact gttattagga 600  
 ctctgtatga tatttggtggc agattgcctt tgtccttcaa aaaggcgag 650  
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 aacctttgaa aaaagtggag gaggaacaag aggcggatga agaagatgtt 750  
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acataaaaagc actaggtata caagtttgaa atatgattta agcacagtat 1050  
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 atttatgtat atttgtttta taataaccta tttcaagtct gagttttgaa 1150  
 aatttacatt tcccaagtat tgcattattg aggtatttaa gaagattatt 1200  
 ttagagaaaa atatttctca tttgatataa ttttctctg tttcactgtg 1250  
 tgaaaaaaag aagatatttc ccataaatgg gaagtttgcc cattgtctca 1300  
 agaaatgtgt atttcagtga caatttcgtg gtcttttttag aggtatattc 1350  
 caaaatttcc ttgtattttt aggttatgca actaataaaa actaccttac 1400  
 attaattaat tacagttttc tacacatggg aatacaggat atgctactga 1450  
 tttaggaagt ttttaagttc atgggtattct cttgattcca acaaagtttg 1500  
 attttctctt gtatttttct tacttactat gggttacatt ttttattttt 1550  
 caaattggat gataatttct tggaaacatt ttttatgttt tagtaaacag 1600  
 tatttttttg ttgtttcaaa ctgaagtta ctgagagatc catcaaattg 1650  
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 caggaaaaag catcttcttg tatatgtctt aaatgtattt ttgtcctcat 1900  
 atacagaaaag ttcttaattg attttacagt ctgtaatgct tgatgtttta 1950  
 aaataataac atttttatat tttttaaaag acaaacttca tattatcctg 2000  
 tgttctttcc tgactggtaa tattgtgtgg gatttcacag gtaaaagtca 2050  
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 ttctttaaag ccctctcctt tagaatttaa aatattgtac cattaaagag 2300  
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aaacctttct aaccatttca ttaaagctga aaaaaaaaaa aaaaaaa 2397

<210> 325

<211> 280

<212> PRT

<213> Homo Sapien

<400> 325

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Ala | Pro | Ser | Gly | Ser | Leu | Ala | Val | Pro | Leu | Ala | Val | Leu | Val | 1   | 5   | 10  | 15 |
| Leu | Leu | Leu | Trp | Gly | Ala | Pro | Trp | Thr | His | Gly | Arg | Arg | Ser | Asn | 20  | 25  | 30  |    |
| Val | Arg | Val | Ile | Thr | Asp | Glu | Asn | Trp | Arg | Glu | Leu | Leu | Glu | Gly | 35  | 40  | 45  |    |
| Asp | Trp | Met | Ile | Glu | Phe | Tyr | Ala | Pro | Trp | Cys | Pro | Ala | Cys | Gln | 50  | 55  | 60  |    |
| Asn | Leu | Gln | Pro | Glu | Trp | Glu | Ser | Phe | Ala | Glu | Trp | Gly | Glu | Asp | 65  | 70  | 75  |    |
| Leu | Glu | Val | Asn | Ile | Ala | Lys | Val | Asp | Val | Thr | Glu | Gln | Pro | Gly | 80  | 85  | 90  |    |
| Leu | Ser | Gly | Arg | Phe | Ile | Ile | Thr | Ala | Leu | Pro | Thr | Ile | Tyr | His | 95  | 100 | 105 |    |
| Cys | Lys | Asp | Gly | Glu | Phe | Arg | Arg | Tyr | Gln | Gly | Pro | Arg | Thr | Lys | 110 | 115 | 120 |    |
| Lys | Asp | Phe | Ile | Asn | Phe | Ile | Ser | Asp | Lys | Glu | Trp | Lys | Ser | Ile | 125 | 130 | 135 |    |
| Glu | Pro | Val | Ser | Ser | Trp | Phe | Gly | Pro | Gly | Ser | Val | Leu | Met | Ser | 140 | 145 | 150 |    |
| Ser | Met | Ser | Ala | Leu | Phe | Gln | Leu | Ser | Met | Trp | Ile | Arg | Thr | Cys | 155 | 160 | 165 |    |
| His | Asn | Tyr | Phe | Ile | Glu | Asp | Leu | Gly | Leu | Pro | Val | Trp | Gly | Ser | 170 | 175 | 180 |    |
| Tyr | Thr | Val | Phe | Ala | Leu | Ala | Thr | Leu | Phe | Ser | Gly | Leu | Leu | Leu | 185 | 190 | 195 |    |
| Gly | Leu | Cys | Met | Ile | Phe | Val | Ala | Asp | Cys | Leu | Cys | Pro | Ser | Lys | 200 | 205 | 210 |    |
| Arg | Arg | Arg | Pro | Gln | Pro | Tyr | Pro | Tyr | Pro | Ser | Lys | Lys | Leu | Leu |     |     |     |    |

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<210> 326
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 326
    tgaggtgggc aagcggcgaa atg 23

<210> 327
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 327
    tatgtggatc aggacgtgcc 20

<210> 328
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 328
    tgcaggggttc agtctagatt g 21

<210> 329
<211> 25
<212> DNA
<213> Artificial Sequence

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<220>

<223> Synthetic Oligonucleotide Probe

<400> 329

ttgaaggaca aaggcaatct gccac 25

<210> 330

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 330

ggagtcttgc agttcccttg gcagtcctgg tgctgttgct ttggg 45

<210> 331

<211> 2168

<212> DNA

<213> Homo Sapien

<400> 331

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 acttccctct gtgaccatga aactctgggt gtctgcattg ctgatggcct 200  
 ggtttggtgt cctgagctgt gtgcaggccg aattcttcac ctctattggg 250  
 cacatgactg acctgattta tgcagagaaa gagctgggtgc agtctctgaa 300  
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 gttagctgtc tagcgcttag caagggtgct ttgtacctca ggtgttttag 2050  
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gtttttatgg catttctatc tattgtggct ttaccaaaaa ataaaatgtc 2150

cctaccagaa aaaaaaaaa 2168

<210> 332

<211> 533

<212> PRT

<213> Homo Sapien

<400> 332

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Lys | Leu | Trp | Val | Ser | Ala | Leu | Leu | Met | Ala | Trp | Phe | Gly | Val | 1   | 5   | 10  | 15 |
| Leu | Ser | Cys | Val | Gln | Ala | Glu | Phe | Phe | Thr | Ser | Ile | Gly | His | Met | 20  | 25  | 30  |    |
| Thr | Asp | Leu | Ile | Tyr | Ala | Glu | Lys | Glu | Leu | Val | Gln | Ser | Leu | Lys | 35  | 40  | 45  |    |
| Glu | Tyr | Ile | Leu | Val | Glu | Glu | Ala | Lys | Leu | Ser | Lys | Ile | Lys | Ser | 50  | 55  | 60  |    |
| Trp | Ala | Asn | Lys | Met | Glu | Ala | Leu | Thr | Ser | Lys | Ser | Ala | Ala | Asp | 65  | 70  | 75  |    |
| Ala | Glu | Gly | Tyr | Leu | Ala | His | Pro | Val | Asn | Ala | Tyr | Lys | Leu | Val | 80  | 85  | 90  |    |
| Lys | Arg | Leu | Asn | Thr | Asp | Trp | Pro | Ala | Leu | Glu | Asp | Leu | Val | Leu | 95  | 100 | 105 |    |
| Gln | Asp | Ser | Ala | Ala | Gly | Phe | Ile | Ala | Asn | Leu | Ser | Val | Gln | Arg | 110 | 115 | 120 |    |
| Gln | Phe | Phe | Pro | Thr | Asp | Glu | Asp | Glu | Ile | Gly | Ala | Ala | Lys | Ala | 125 | 130 | 135 |    |
| Leu | Met | Arg | Leu | Gln | Asp | Thr | Tyr | Arg | Leu | Asp | Pro | Gly | Thr | Ile | 140 | 145 | 150 |    |
| Ser | Arg | Gly | Glu | Leu | Pro | Gly | Thr | Lys | Tyr | Gln | Ala | Met | Leu | Ser | 155 | 160 | 165 |    |
| Val | Asp | Asp | Cys | Phe | Gly | Met | Gly | Arg | Ser | Ala | Tyr | Asn | Glu | Gly | 170 | 175 | 180 |    |
| Asp | Tyr | Tyr | His | Thr | Val | Leu | Trp | Met | Glu | Gln | Val | Leu | Lys | Gln | 185 | 190 | 195 |    |
| Leu | Asp | Ala | Gly | Glu | Glu | Ala | Thr | Thr | Thr | Lys | Ser | Gln | Val | Leu | 200 | 205 | 210 |    |

|   |   |     |     |     |
|---|---|-----|-----|-----|
| Asp Tyr Leu Ser   | Tyr Ala Val Phe Gln Leu Gly Asp Leu His Arg | 215 | 220 | 225 |
| Ala Leu Glu Leu Thr Arg Arg Leu Leu Ser Leu Asp Pro Ser His |   | 230 | 235 | 240 |
| Glu Arg Ala Gly Gly Asn Leu Arg Tyr Phe Glu Gln Leu Leu Glu |   | 245 | 250 | 255 |
| Glu Glu Arg Glu Lys Thr Leu Thr Asn Gln Thr Glu Ala Glu Leu |   | 260 | 265 | 270 |
| Ala Thr Pro Glu Gly Ile Tyr Glu Arg Pro Val Asp Tyr Leu Pro |   | 275 | 280 | 285 |
| Glu Arg Asp Val Tyr Glu Ser Leu Cys Arg Gly Glu Gly Val Lys |   | 290 | 295 | 300 |
| Leu Thr Pro Arg Arg Gln Lys Arg Leu Phe Cys Arg Tyr His His |   | 305 | 310 | 315 |
| Gly Asn Arg Ala Pro Gln Leu Leu Ile Ala Pro Phe Lys Glu Glu |   | 320 | 325 | 330 |
| Asp Glu Trp Asp Ser Pro His Ile Val Arg Tyr Tyr Asp Val Met |   | 335 | 340 | 345 |
| Ser Asp Glu Glu Ile Glu Arg Ile Lys Glu Ile Ala Lys Pro Lys |   | 350 | 355 | 360 |
| Leu Ala Arg Ala Thr Val Arg Asp Pro Lys Thr Gly Val Leu Thr |   | 365 | 370 | 375 |
| Val Ala Ser Tyr Arg Val Ser Lys Ser Ser Trp Leu Glu Glu Asp |   | 380 | 385 | 390 |
| Asp Asp Pro Val Val Ala Arg Val Asn Arg Arg Met Gln His Ile |   | 395 | 400 | 405 |
| Thr Gly Leu Thr Val Lys Thr Ala Glu Leu Leu Gln Val Ala Asn |   | 410 | 415 | 420 |
| Tyr Gly Val Gly Gly Gln Tyr Glu Pro His Phe Asp Phe Ser Arg |   | 425 | 430 | 435 |
| Arg Pro Phe Asp Ser Gly Leu Lys Thr Glu Gly Asn Arg Leu Ala |   | 440 | 445 | 450 |
| Thr Phe Leu Asn Tyr Met Ser Asp Val Glu Ala Gly Gly Ala Thr |   | 455 | 460 | 465 |
| Val Phe Pro Asp Leu Gly Ala Ala Ile Trp Pro Lys Lys Gly Thr |   | 470 | 475 | 480 |

09505056-071204

Ala Val Phe Trp Tyr Asn Leu Leu Arg Ser Gly Glu Gly Asp Tyr  
485 490 495

Arg Thr Arg His Ala Ala Cys Pro Val Leu Val Gly Cys Lys Trp  
500 505 510

Val Ser Asn Lys Trp Phe His Glu Arg Gly Gln Glu Phe Leu Arg  
515 520 525

Pro Cys Gly Ser Thr Glu Val Asp  
530

<210> 333

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 333

ccaggcacaa tttccaga 18

<210> 334

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 334

ggacccttct gtgtgccag 19

<210> 335

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 335

ggtctcaaga actcctgtc 19

<210> 336

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

09905056 041201



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<211> 772

<212> PRT

<213> Homo Sapien

<400> 339

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| Met | Arg | Leu | Ser | Ser | Leu | Leu | Ala | Leu | Leu | Arg | Pro | Ala | Leu | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ile | Leu | Gly | Leu | Ser | Leu | Gly | Cys | Ser | Leu | Ser | Leu | Leu | Arg |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ser | Trp | Ile | Gln | Gly | Glu | Gly | Glu | Asp | Pro | Cys | Val | Glu | Ala |
|     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Gly | Glu | Arg | Gly | Gly | Pro | Gln | Asn | Pro | Asp | Ser | Arg | Ala | Arg |
|     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Asp | Gln | Ser | Asp | Glu | Asp | Phe | Lys | Pro | Arg | Ile | Val | Pro | Tyr |
|     |     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Arg | Asp | Pro | Asn | Lys | Pro | Tyr | Lys | Lys | Val | Leu | Arg | Thr | Arg |
|     |     |     |     | 80  |     |     |     |     | 85  |     |     |     |     | 90  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Ile | Gln | Thr | Glu | Leu | Gly | Ser | Arg | Glu | Arg | Leu | Leu | Val | Ala |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

|                 |                     |                         |     |  |     |
|-----------------|---------------------|-------------------------|-----|--|-----|
|                 | 95                  |                         | 100 |  | 105 |
| Val Leu Thr Ser | Arg Ala Thr Leu Ser | Thr Leu Ala Val Ala Val |     |  |     |
|                 | 110                 |                         | 115 |  | 120 |
| Asn Arg Thr Val | Ala His His Phe Pro | Arg Leu Leu Tyr Phe Thr |     |  |     |
|                 | 125                 |                         | 130 |  | 135 |
| Gly Gln Arg Gly | Ala Arg Ala Pro Ala | Gly Met Gln Val Val Ser |     |  |     |
|                 | 140                 |                         | 145 |  | 150 |
| His Gly Asp Glu | Arg Pro Ala Trp Leu | Met Ser Glu Thr Leu Arg |     |  |     |
|                 | 155                 |                         | 160 |  | 165 |
| His Leu His Thr | His Phe Gly Ala Asp | Tyr Asp Trp Phe Phe Ile |     |  |     |
|                 | 170                 |                         | 175 |  | 180 |
| Met Gln Asp Asp | Thr Tyr Val Gln Ala | Pro Arg Leu Ala Ala Leu |     |  |     |
|                 | 185                 |                         | 190 |  | 195 |
| Ala Gly His Leu | Ser Ile Asn Gln Asp | Leu Tyr Leu Gly Arg Ala |     |  |     |
|                 | 200                 |                         | 205 |  | 210 |
| Glu Glu Phe Ile | Gly Ala Gly Glu Gln | Ala Arg Tyr Cys His Gly |     |  |     |
|                 | 215                 |                         | 220 |  | 225 |
| Gly Phe Gly Tyr | Leu Leu Ser Arg Ser | Leu Leu Leu Arg Leu Arg |     |  |     |
|                 | 230                 |                         | 235 |  | 240 |
| Pro His Leu Asp | Gly Cys Arg Gly Asp | Ile Leu Ser Ala Arg Pro |     |  |     |
|                 | 245                 |                         | 250 |  | 255 |
| Asp Glu Trp Leu | Gly Arg Cys Leu Ile | Asp Ser Leu Gly Val Gly |     |  |     |
|                 | 260                 |                         | 265 |  | 270 |
| Cys Val Ser Gln | His Gln Gly Gln Gln | Tyr Arg Ser Phe Glu Leu |     |  |     |
|                 | 275                 |                         | 280 |  | 285 |
| Ala Lys Asn Arg | Asp Pro Glu Lys Glu | Gly Ser Ser Ala Phe Leu |     |  |     |
|                 | 290                 |                         | 295 |  | 300 |
| Ser Ala Phe Ala | Val His Pro Val Ser | Glu Gly Thr Leu Met Tyr |     |  |     |
|                 | 305                 |                         | 310 |  | 315 |
| Arg Leu His Lys | Arg Phe Ser Ala Leu | Glu Leu Glu Arg Ala Tyr |     |  |     |
|                 | 320                 |                         | 325 |  | 330 |
| Ser Glu Ile Glu | Gln Leu Gln Ala Gln | Ile Arg Asn Leu Thr Val |     |  |     |
|                 | 335                 |                         | 340 |  | 345 |
| Leu Thr Pro Glu | Gly Glu Ala Gly Leu | Ser Trp Pro Val Gly Leu |     |  |     |
|                 | 350                 |                         | 355 |  | 360 |



Ser Pro Gln Arg Ser Pro Pro Gly Pro Pro Gly Ala Gly Pro Asp  
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 Pro Pro Ser Pro Pro Gly Ala Asp Pro Ser Arg Gly Ala Pro Ile  
 650 655 660  
 Gly Gly Arg Phe Asp Arg Gln Ala Ser Ala Glu Gly Cys Phe Tyr  
 665 670 675  
 Asn Ala Asp Tyr Leu Ala Ala Arg Ala Arg Leu Ala Gly Glu Leu  
 680 685 690  
 Ala Gly Gln Glu Glu Glu Glu Ala Leu Glu Gly Leu Glu Val Met  
 695 700 705  
 Asp Val Phe Leu Arg Phe Ser Gly Leu His Leu Phe Arg Ala Val  
 710 715 720  
 Glu Pro Gly Leu Val Gln Lys Phe Ser Leu Arg Asp Cys Ser Pro  
 725 730 735  
 Arg Leu Ser Glu Glu Leu Tyr His Arg Cys Arg Leu Ser Asn Leu  
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 tgctaggaca cattaggatt ggtcatggaa atagaatgca ccaccatgag 200  
 catcatcacc tacaagctcc taacaaagaa gatatcttga aaatttcaga 250  
 ggatgagcgc atggagctca gtaagagctt tcgagtatac tgtattatcc 300  
 ttgtaaaacc caaagatgtg agtctttggg ctgcagtaaa ggagacttgg 350  
 accaaacact gtgacaaagc agagttcttc agttctgaaa atgttaaagt 400

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 aagcttacaa atacgccttt gataagtata gagaccaata caactgggtc 500  
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<211> 318

<212> PRT

<213> Homo Sapien

&lt;400&gt; 341

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| Met | Leu | Ser | Glu | Ser | Ser | Ser | Phe | Leu | Lys | Gly | Val | Met | Leu | Gly | 1   | 5   | 10  | 15 |
| Ser | Ile | Phe | Cys | Ala | Leu | Ile | Thr | Met | Leu | Gly | His | Ile | Arg | Ile | 20  | 25  | 30  |    |
| Gly | His | Gly | Asn | Arg | Met | His | His | His | Glu | His | His | His | Leu | Gln | 35  | 40  | 45  |    |
| Ala | Pro | Asn | Lys | Glu | Asp | Ile | Leu | Lys | Ile | Ser | Glu | Asp | Glu | Arg | 50  | 55  | 60  |    |
| Met | Glu | Leu | Ser | Lys | Ser | Phe | Arg | Val | Tyr | Cys | Ile | Ile | Leu | Val | 65  | 70  | 75  |    |
| Lys | Pro | Lys | Asp | Val | Ser | Leu | Trp | Ala | Ala | Val | Lys | Glu | Thr | Trp | 80  | 85  | 90  |    |
| Thr | Lys | His | Cys | Asp | Lys | Ala | Glu | Phe | Phe | Ser | Ser | Glu | Asn | Val | 95  | 100 | 105 |    |
| Lys | Val | Phe | Glu | Ser | Ile | Asn | Met | Asp | Thr | Asn | Asp | Met | Trp | Leu | 110 | 115 | 120 |    |
| Met | Met | Arg | Lys | Ala | Tyr | Lys | Tyr | Ala | Phe | Asp | Lys | Tyr | Arg | Asp | 125 | 130 | 135 |    |
| Gln | Tyr | Asn | Trp | Phe | Phe | Leu | Ala | Arg | Pro | Thr | Thr | Phe | Ala | Ile | 140 | 145 | 150 |    |
| Ile | Glu | Asn | Leu | Lys | Tyr | Phe | Leu | Leu | Lys | Lys | Asp | Pro | Ser | Gln | 155 | 160 | 165 |    |
| Pro | Phe | Tyr | Leu | Gly | His | Thr | Ile | Lys | Ser | Gly | Asp | Leu | Glu | Tyr | 170 | 175 | 180 |    |
| Val | Gly | Met | Glu | Gly | Gly | Ile | Val | Leu | Ser | Val | Glu | Ser | Met | Lys | 185 | 190 | 195 |    |
| Arg | Leu | Asn | Ser | Leu | Leu | Asn | Ile | Pro | Glu | Lys | Cys | Pro | Glu | Gln | 200 | 205 | 210 |    |
| Gly | Gly | Met | Ile | Trp | Lys | Ile | Ser | Glu | Asp | Lys | Gln | Leu | Ala | Val | 215 | 220 | 225 |    |
| Cys | Leu | Lys | Tyr | Ala | Gly | Val | Phe | Ala | Glu | Asn | Ala | Glu | Asp | Ala | 230 | 235 | 240 |    |
| Asp | Gly | Lys | Asp | Val | Phe | Asn | Thr | Lys | Ser | Val | Gly | Leu | Ser | Ile | 245 | 250 | 255 |    |
| Lys | Glu | Ala | Met | Thr | Tyr | His | Pro | Asn | Gln | Val | Val | Glu | Gly | Cys |     |     |     |    |

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T03T20 95050560



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gcccaaattgc cctaaggcgg tatacccc 28

<211> 50

<213> Artificial Sequence

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<210> 346

<211> 25

<212> DNA

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<210> 348

<211> 48

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TEB 40 9305050

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<210> 369

<211> 48

<212> DNA

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| Lys | Asp | Asp | Ser | Gly | Gln | Tyr | Tyr | Cys | Ile | Ala | Ser | Asn | Asp | Ala |
|     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     | 225 |
| Gly | Ser | Ala | Arg | Cys | Glu | Glu | Gln | Glu | Met | Glu | Val | Tyr | Asp | Leu |
|     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Asn | Ile | Gly | Gly | Ile | Ile | Gly | Gly | Val | Leu | Val | Val | Leu | Ala | Val |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |
| Leu | Ala | Leu | Ile | Thr | Leu | Gly | Ile | Cys | Cys | Ala | Tyr | Arg | Arg | Gly |
|     |     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |
| Tyr | Phe | Ile | Asn | Asn | Lys | Gln | Asp | Gly | Glu | Ser | Tyr | Lys | Asn | Pro |
|     |     |     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |
| Gly | Lys | Pro | Asp | Gly | Val | Asn | Tyr | Ile | Arg | Thr | Asp | Glu | Glu | Gly |
|     |     |     |     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |
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